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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 22.8974 Seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LQKLSLPETGELDSATLKA.....VPLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	707	3	US-08-704-711A-19
2	258	100.0	707	3	US-09-521-220-19
3	258	100.0	707	3	US-09-391-104-20
4	258	100.0	707	4	US-09-949-016-6575
5	258	100.0	708	3	US-08-448-489-16
6	258	100.0	708	4	US-09-689-730-16
7	258	100.0	713	4	US-09-949-016-10629
8	141	54.7	477	3	US-08-704-711A-20
9	141	54.7	477	3	US-08-448-489-15
10	141	54.7	477	3	US-08-281-313-1
11	141	54.7	477	3	US-09-521-220-20
12	141	54.7	477	3	US-09-391-104-21
13	141	54.7	477	4	US-09-689-730-15
14	133	51.6	476	3	US-08-704-711A-21
15	133	51.6	476	3	US-08-448-489-14
16	133	51.6	476	3	US-09-521-220-21
17	133	51.6	476	3	US-09-391-104-22
18	133	51.6	476	4	US-09-949-016-6224
19	133	51.6	476	4	US-09-689-730-14
20	133	51.6	484	4	US-09-949-016-10877
21	117	45.3	471	3	US-09-391-104-25
22	117	45.3	480	4	US-09-949-016-10560
23	115	44.6	136	4	US-09-513-999C-4639
24	115	44.6	663	4	US-09-194-468A-30
25	114	44.2	631	3	US-08-448-489-17
26	114	44.2	631	4	US-09-689-730-17
27	114	44.2	660	3	US-08-704-711A-18

28	114	44.2	660	3	US-09-521-220-18	Sequence 18, Appl
29	114	44.2	660	3	US-09-391-104-19	Sequence 19, Appl
30	114	44.2	660	4	US-09-917-254-89	Sequence 89, Appl
31	114	44.2	660	4	US-09-949-016-6512	Sequence 6512, Ap
32	114	44.2	660	4	US-09-949-016-7937	Sequence 7937, Ap
33	113	43.8	470	3	US-08-668-392-2	Sequence 2, Appl
34	113	43.8	470	3	US-08-396-988-2	Sequence 2, Appl
35	113	43.8	470	3	US-09-391-104-26	Sequence 26, Appl
36	113	43.8	473	4	US-09-949-016-10876	Sequence 10876, A
37	110	42.6	469	3	US-08-704-711A-16	Sequence 16, Appl
38	110	42.6	469	3	US-08-448-489-12	Sequence 12, Appl
39	110	42.6	469	3	US-09-521-220-16	Sequence 16, Appl
40	110	42.6	469	3	US-09-391-104-23	Sequence 23, Appl
41	110	42.6	469	4	US-09-949-016-6223	Sequence 6223, Ap
42	110	42.6	469	4	US-09-689-730-12	Sequence 12, Appl
43	110	42.6	491	4	US-09-949-016-10875	Sequence 10875, A
44	109	42.2	513	4	US-09-862-631-4	Sequence 4, Appl
45	108	41.9	471	4	US-08-994-689C-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-704-711A-19
; Sequence 19, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683.
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 9041136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 707 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-19

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 2

US-09-521-220-19
 ; Sequence 19, Application US/09521220
 ; Patent No. 639348
 ; GENERAL INFORMATION:
 ; APPLICANT: WILL, Horst
 ; INVENTOR: HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; METALLOPROTEASES, THEIR PRODUCTION AND USE
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/521,220
 ; FILING DATE: 08-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; 21-OCT-1994
 ; 17-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/704,711
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: DE 4438838.1
 ; FILING DATE: 21-OCT-1994
 ; APPLICATION NUMBER: DE 4409663.1
 ; FILING DATE: 17-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GRANADOS, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 26083/124
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; INFORMATION FOR SEQ ID NO: 19:
 ; TYPE: amino acid
 ; LENGTH: 707 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 3

US-09-391-104-20

; Sequence 20, Application US/093911104
 ; Patent No. 639371
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Falduto, Michael T.
 ; APPLICANT: Magnuson, Scott R.
 ; APPLICANT: Morgan, Douglas W.
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
 ; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
 ; TITLE OF INVENTION: OF USING SAME
 ; FILE REFERENCE: 6073.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/391,104
 ; PRIOR FILING DATE: 1999-09-07
 ; PRIOR APPLICATION NUMBER: US 08/814,394
 ; PRIOR FILING DATE: 1997-03-11
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 20
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-391-104-20

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 4

US-09-949-016-6575
 ; Sequence 6575, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6575
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-6575

Query Match 100.0%; Score 258; DB 4; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMTRPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 5

US-08-448-489-16
 ; Sequence 16, Application US/08448489
 ; Patent No. 6184022
 ; GENERAL INFORMATION:
 ; APPLICANT: SEIKI, Motoharu
 ; APPLICANT: SATO, Hiroshi

Amend 2/6/01

APPLICANT: SHINAGAWA, Akira
 TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
 FILE REFERENCE: 55-290P
 CURRENT APPLICATION NUMBER: US/08/448,489
 CURRENT FILING DATE: 1995-06-07
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO 16
 LENGTH: 708
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: X = UNKNOWN
 OTHER INFORMATION: Description of Unknown Organism: Known Member of
 OTHER INFORMATION: Matrix Metalloproteinase Family
 US-08-448-489-16

Query Match 100.0%; Score 258; DB 3; Length 708;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 120

RESULT 6

US-09-689-730-16
 Sequence 16, Application US/09689730
 Patent No. 6825024
 GENERAL INFORMATION:
 APPLICANT: SEIKI, Motoharu
 APPLICANT: SATO, Hiroshi
 APPLICANT: SHINAGAWA, Akira
 TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
 FILE REFERENCE: 55-290P
 CURRENT APPLICATION NUMBER: US/09/689,730
 CURRENT FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: US/08/448,489
 PRIOR FILING DATE: 1995-06-07
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO 16
 LENGTH: 708
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: X = UNKNOWN
 OTHER INFORMATION: Description of Unknown Organism: Known Member of
 OTHER INFORMATION: Matrix Metalloproteinase Family
 US-09-689-730-16

Query Match 100.0%; Score 258; DB 4; Length 708;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 120

RESULT 7

US-09-949-016-10629
 Sequence 10629, Application US/09949016
 Patent No. 9812332
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10629
 LENGTH: 713
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-10629

Query Match 100.0%; Score 258; DB 4; Length 713;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 47
 Db 80 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTEGDLKWHHN 126

RESULT 8

US-08-704-711A-20
 Sequence 20, Application US/08704711A
 Patent No. 6114159
 GENERAL INFORMATION:
 APPLICANT: WILLY, Horst
 APPLICANT: HINZMANN, Bernd
 TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 METALLOPROTEASES, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/704,711A
 FILING DATE: 20-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/DE95/00357
 FILING DATE: 17-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 4409663.1
 FILING DATE: 17-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: GRANADOS, Patricia D.
 REGISTRATION NUMBER: 33,683
 REFERENCE/DOCKET NUMBER: 26083/124
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 477 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-704-711A-20

No d's to Prod.
 D Products w/
 Repl.

Gen out w/ 3 mutations del Rej.

Prod. w/

Labels ← Cl. 3 1-173 No.

Cl. 1

No Comp. w/

Mo. w/

drawings

↑ Same as, only

Cl's to DNA, & Repl. Part.

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 11

US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-521-220-20

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 12

US-09-391-104-21
; Sequence 21, Application US/09391104

; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-21

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 13

US-09-689-730-15
; Sequence 15, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-15

Query Match 54.7%; Score 141; DB 4; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVPDVGHFRTFPGIPKW 109

RESULT 14

US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX

;; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/704,711A
;; FILING DATE: 20-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/DE95/00357
;; FILING DATE: 17-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE 4438838.1
;; FILING DATE: 21-OCT-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE 4409663.1
;; FILING DATE: 17-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 26083/124
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 476 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-704-711A-21

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.9e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLTLEVMRKPRCGVDPDVGHFSFPGMPKW 108

RESULT 15
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family

US-08-448-489-14
Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.9e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 1 LOKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDLTLEVMRKPRCGVDPDVGHFSFPGMPKW 108

Search completed: May 27, 2005, 06:47:41
Job time : 23.8974 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 91.2885 Seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQKQLSLPETGELDSLTKA.....VPLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP97130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	6	ADQ17091 Human mat
4	258	100.0	432	5	ABP69247 Human pol
5	258	100.0	702	5	ABP69246 Human pol
6	258	100.0	707	2	AAR07077 92-kDa hu
7	258	100.0	707	3	AAY58015 Matrix me
8	258	100.0	707	4	AAB84611 Amino aci
9	258	100.0	707	4	AAE10432 Human mat
10	258	100.0	707	4	AAB20491 Human mat
11	258	100.0	707	6	ABU56680 Lung canc
12	258	100.0	707	6	ABU56467 Lung canc
13	258	100.0	707	6	AAO16609 Human mat
14	258	100.0	707	6	ABR92116 Human cer
15	258	100.0	707	7	ADL14993 Human typ
16	258	100.0	707	7	ADN39040 Cancer/an
17	258	100.0	707	7	ADN39935 Cancer/an
18	258	100.0	707	8	ADH17067 Human mat
19	258	100.0	707	8	ADJ75581 Marker ge
20	258	100.0	707	8	ADM67186 Human adi
21	258	100.0	707	8	ADN07701 Human mat
22	258	100.0	707	8	ADQ19168 Human sof
23	258	100.0	707	8	ABM82250 Tumour-as
24	258	100.0	707	8	ADP54466 Human PRO
25	258	100.0	707	8	ADP23624 PRO polyp

26	258	100.0	707	8	ADQ39936 Human myo
27	258	100.0	707	8	ADL17080 Human 173
28	228	88.4	43	6	ABP97138 Human mat
29	228	88.4	43	6	ABG76324 Partial s
30	228	88.4	43	8	ADQ17099 Human mat
31	213.5	82.8	730	8	ADJ76307 Marker ge
32	213.5	82.8	730	8	ADH85049 Mouse ato
33	150	58.1	171	5	ABG31461 Peptidase
34	141	54.7	54	6	ABP97127 Human mat
35	141	54.7	54	6	ABG76313 Human mat
36	141	54.7	54	8	ADQ17088 Human mat
37	141	54.7	460	1	AAP93629 Sequence
38	141	54.7	477	2	AAY21993 Human mat
39	141	54.7	477	2	AAY21994 Human mat
40	141	54.7	477	4	AAH84608 Amino aci
41	141	54.7	477	4	AAE10420 Human mat
42	141	54.7	477	4	AAO20482 Proetrome
43	141	54.7	477	5	ABO4752 Human MMP
44	141	54.7	477	6	ABP72353 Matrix me
45	141	54.7	477	6	ABU03473 Angiogene

ALIGNMENTS

RESULT 1

ABP97130

ID ABP97130 standard; peptide; 47 AA.

XX AC ABP97130;

XX XX 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW KW matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant;
KW KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX PN WO2003018748-A2.

XX XX 06-MAR-2003.

XX PD 15-AUG-2002; 2002WO-US026319.

XX PF 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX XX Quirk S, Weart IF;

XX XX WPI; 2003-381408/36.

XX DR Anti-angiogenic composition comprising peptide inhibitor of matrix
XX PT metalloproteinase, useful for decreasing the expression of vascular
XX PT endothelial growth factor and treating cancers and tissue injuries.
XX XX Claim 17; Page 16; 103pp; English.

XX PS The present invention describes an anti-angiogenic composition (I) for
XX CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)
XX CC comprises an effective amount of a peptide inhibitor of matrix
XX CC metalloproteinase (MMP), where the peptide can inhibit the expression of
XX CC VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,
XX CC antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (1) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;
 Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 2

ABG76316
 ID ABG76316 standard; protein; 47 AA.

AC ABG76316;

XX DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating and preventing scarring, improving skin tone,
 CC reducing wrinkling and for stimulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 3

ADQ17091
 ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIRK/) QUIRK S.

XX PI Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 8; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 4

ABP69247

ID ABP69247 standard; protein; 432 AA.

XX AC ABP69247;

XX DT 20-JAN-2003 (first entry)

DE XX Human polypeptide SEQ ID NO 1294.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX antiarthritic.

XX Homo sapiens.

XX WO200270539-A2. = VS 6, 783, 969 B1

XX 12-SEP-2002. Not Pub. in time

XX 05-MAR-2002; 2002WO-US005095.

XX 05-MAR-2001; 2001US-00799451. 3/5/01 PD

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AU, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;
XX WPI; 2002-759812/82.
XX N-PSDB; ABZ11464.

XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.

XX Claim 9; SEQ ID NO 1294; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 432 AA;

Query Match 100.0%; Score 258; DB 5; Length 432;
Best Local Similarity 100.0%; Pred. No. 5e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQQLSLPETGELDSATLKAMRTPRCVPLDGRFQTPEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCVPLDGRFQTPEGDLKWHHN 120

RESULT 5
ID ABP69246
XX ABP69246;
XX ABP69246;
XX 20-JAN-2003 (first entry)
DT

DE XX Human polypeptide SEQ ID NO 1293.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX antiarthritic.

XX Homo sapiens.

XX WO200270539-A2. = 6, 783, 969 B1

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AU, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;
XX WPI; 2002-759812/82.
XX N-PSDB; ABZ11463.

XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.

XX Claim 9; SEQ ID NO 1293; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 702 AA;

Query Match 100.0%; Score 258; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 9.1e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQQLSLPETGELDSATLKAMRTPRCVPLDGRFQTPEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCVPLDGRFQTPEGDLKWHHN 120

RESULT 6
ID AAR07077
XX AAR07077;
XX AAR07077;
XX 25-MAR-2003 (revised)
DT 19-FEB-1991 (first entry)

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XX DE 92-kDa human type IV collagenase gene product.
XX KW Epidermal growth factor; EGF; interleukin 1; IL-1; tumour TPA.
XX OS Homo sapiens.
XX FH Key
XX FT Protein
XX FT /label= Mature protein
XX FT Active-site
XX FT /label= Glycosylation site
XX FT Active-site
XX FT /label= Glycosylation site
XX FT Active-site
XX FT /label= Glycosylation site
XX PN EP398859-A.
XX XX
XX PD 22-NOV-1990.
XX PF 14-MAY-1990; 90EP-00870069.
XX PR 15-MAY-1989; 89US-00352078.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Goldberg GI, Eisen AZ;
XX DR WPI; 1990-350579/47.
XX DR N-PSDB; AAQ06554.
XX XX
XX PT New 92-kD type IV collagenase and cDNA - from SV-40 transformed foetal
XX PT lung fibroblasts.
XX PS Claim 1; Fig 3; 21pp; English.
XX CC SV40 transformed foetal lung fibroblasts may be used to produce type IV
XX CC collagenase, totally glycosylated at three sites. The enzyme is induced
XX CC by EGF, IL-2 and the tumour promoter, 12-O-tetradecanoyl- phorbol acetate
XX CC (TPA) and has therapeutic activity, being able to digest native type IV
XX CC and V collagen. (Updated on 25-MAR-2003 to correct PA field.)
XX XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 2; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 7
AAY58015
ID AAY58015 standard; protein; 707 AA.
XX AC
XX AC AAY58015;
XX DT 28-FEB-2000 (first entry)
XX DE
XX XX Matrix metalloproteinase-9 (MMP-9) amino acid sequence.
XX KW Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;
XX KW inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;
XX KW neurological disease; multiple sclerosis; arthritis; human.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO957315-A2.
XX XX
XX PD 11-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001447.
XX PR 07-MAY-1998; 98GB-00009764.
XX PA (ISIS-) ISIS INNOVATION LTD.
XX PI Zhang BP, Ye S, Henney A;
XX FT WPI; 2000-052977/04.
XX DR N-PSDB; AA245145.
XX PT Detection of matrix metalloprotease 9 gene polymorphisms for diagnosis or
XX PT prognosis of diseases characterized by metalloproteinase mediated
XX PT remodelling.
XX PS Example 1; Fig 1; 29pp; English.
XX CC This is the human matrix metalloproteinase-9 (MMP-9) amino acid sequence.
XX CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.
XX CC MMP activity is associated with inflammatory diseases and MMP-9 is
XX CC implicated in the pathology of multiple sclerosis. Certain polymorphic
XX CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated
XX CC region of the human MMP-9 gene can affect the severity of
XX CC atherosclerosis. The invention relates to the presence or absence of one
XX CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),
XX CC detection of this polymorphism using oligonucleotides AAZ45137-245140 can
XX CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T
XX CC polymorphism is a regulatory functional polymorphism. The methods and
XX CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They
XX CC are useful for the diagnosis and prognosis of diseases characterized by
XX CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour
XX CC invasion and metastasis, inflammatory disease, and neurological diseases,
XX CC particularly those involving demyelination such as multiple sclerosis,
XX CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be
XX CC used for screening compounds that bind specifically to a molecule encoded
XX CC by one variant of a polymorphic sequence, thus identifying compounds
XX CC which modulate the activity of the enzyme. Such compounds can then be
XX CC used for rational drug design
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 8
AAB84611
ID AAB84611 standard; protein; 707 AA.
XX AC
XX AC AAB84611;
XX DT 05-SEP-2001 (first entry)
XX DE
XX XX Amino acid sequence of matrix metalloproteinase-9.
XX KW Growth factor; protein inhibitor; protease; damaged tissue;
XX KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
XX KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
XX KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
XX KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
XX KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
XX KW vascular endothelial growth factor; urokinase plasminogen activator;
XX KW dermal ulcer; wound.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200149309-A2.

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PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Romanic Arnold A, Barone FC, Bingham S;
XX
XX WPI; 2001-290654/30.
XX
XX DR N-PSDB; AAF30808.
XX
XX PT Polypeptide for the treatment of pain and the reduction of tissue damage
XX PT comprises an inhibitor of human matrix metalloproteinase.
XX
XX PS Claim 1; Fig 4; 61pp; English.
XX
XX CC The present sequence is that of human matrix metalloproteinase-9 (MMP-9),
XX CC previously known as 92 kDa gelatinase and gelatinase B. MMP-9 is capable
XX CC of degrading the extracellular matrix components of the basement
XX CC membrane. The invention relates to methods for treating pain in a patient
XX CC by administering a dual inhibitor of MMP-9 and MMP-2 (see AAB20490). The
XX CC administration of an inhibitor of MMP-9 is useful for treating nerve
XX CC tissue damage (claimed), where the patient is suffering from a disease or
XX CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
XX CC ischaemia and cerebral infarction (claimed). The method is useful for
XX CC treating a disease, disorder or nerve tissue damage selected from
XX CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
XX CC facial pain, neuropathic pain, back pain, complex regional pain syndrome
XX CC I and II, arthritic pain, sports injury pain, pain related to virus
XX CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,
XX CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
XX CC pain, physiological pain, inflammatory pain, acute inflammatory
XX CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,
XX CC traumatic nerve injury, and tolerance to narcotics or withdrawal from
XX CC narcotics (claimed). MMP-9 polypeptides can also be used to screen for
XX CC agonist or antagonist (inhibitor) compounds
XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 4; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 11
ABU56680
ID ABU56680 standard; protein; 707 AA.
XX
XX AC ABU56680;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Lung cancer-associated polypeptide #273.
XX
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX OS Unidentified.
XX
XX PN WO200286443-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 18-APR-2002; 2002WO-US012476.
XX
XX PR 18-APR-2001; 2001US-0284770P.
XX
XX PR 10-MAY-2001; 2001US-0290492P.
XX
XX PR 09-NOV-2001; 2001US-0339245P.
XX
XX PR 13-NOV-2001; 2001US-0350666P.
XX
XX PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.
XX
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX PI Aziz N, Murray R;
XX
XX DR WPI; 2003-093161/08.
XX
XX DR N-PSDB; ABX76409.
XX
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer.
XX
XX PS Claim 27; Page 398; 453pp; English.
XX
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridises
XX CC to a sequence that is at least 80 % identical to a gene that exhibits
XX CC increased or decreased expression in lung cancer samples. Lung cancer-
XX CC associated polynucleotides and polypeptides are used for identifying a
XX CC compound that modulates a lung cancer-associated polypeptide, for
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung
XX CC cancer in a patient and for treating a mammal having lung cancer by
XX CC administering a modulatory compound identified. The methods are useful
XX CC for treating lung cancer, such as small cell lung cancer, non-small cell
XX CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX CC for diagnostic purposes and as targets for screening for therapeutic
XX CC compounds that modulate lung cancer, such as antibodies. Sequences
XX CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
XX CC invention
XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 12
ABU56467
ID ABU56467 standard; protein; 707 AA.
XX
XX AC ABU56467;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Lung cancer-associated polypeptide #60.
XX
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX OS Unidentified.
XX
XX PN WO200286443-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 18-APR-2002; 2002WO-US012476.
XX
XX PR 18-APR-2001; 2001US-0284770P.
XX
XX PR 10-MAY-2001; 2001US-0290492P.

```


PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI Gannavarapu M, Glatt K, Hoersch S;
XX
XX WPI; 2003-156967/15.
DR N-PSDB; ACF12899.
XX
XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
XX Claim 4; Page 294-295; 386pp; English.
XX
XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (I) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
XX SQ Sequence 707 AA;
Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQQLSLPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120
RESULT 15
ADL14993
ID ADL14993 standard; protein; 707 AA.
XX
XX AC ADL14993;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human type IV collagenase protein for cancer treatment.
XX
XX KW cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;
XX KW prognosis; mantle cell lymphoma; cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO2003068268-A2.
XX
XX PD 21-AUG-2003.
XX
XX PF 13-FEB-2003; 2003WO-EP001461.
XX
XX PR 14-FEB-2002; 2002GB-00003480.
XX PR 29-JUN-2002; 2002GB-00015095.
XX
XX PA (BIOI-) BIOINVENT INT AB.
XX
XX PI Ek S, Borrebaeck CAK, Ehinger M;
XX
XX DR WPI; 2003-697496/66.
XX DR N-PSDB; ADL14994.
XX
XX PT New compound for treating, imaging, diagnosing or prognosing mantle cell
PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.
PT

PT nucleic acid).
XX
XX Disclosure; SEQ ID NO 5; 342pp; English.
XX
XX The invention relates to a compound comprising a binding moiety which
CC selectively binds to a protein or polypeptide listed in the specification
CC (e.g. human autotaxin polypeptide or human CD24 signal transducer
CC polypeptide), and a further moiety. The compound is useful in medicine or
CC in the treatment, imaging, diagnosis or prognosis of mantle cell
CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC in the body of an individual. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
XX SQ Sequence 707 AA;
Query Match 100.0%; Score 258; DB 7; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQQLSLPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120
Search completed: May 27, 2005, 06:52:53
Job time : 95.2885 secs

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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:53:10 ; Search time 273.564 Seconds
(without alignments)

59.268 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LKQLSLPFGELDSATLKA.....VPLGRFQTPEGLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	258	100.0	47 14	US-10-219-329-8
2	258	100.0	47 14	US-10-153-185-8
3	258	100.0	47 14	US-10-219-561-8
4	258	100.0	47 16	US-10-032-376A-8
5	258	100.0	47 16	US-10-335-207-8
6	258	100.0	707 9	US-09-391-104-20
7	258	100.0	707 9	US-09-801-196-36
8	258	100.0	707 14	US-10-171-311-142
9	258	100.0	707 14	US-10-301-822-132
10	258	100.0	707 14	US-10-131-985-33
11	258	100.0	707 15	US-10-295-027-358
12	258	100.0	707 15	US-10-295-027-1253
13	258	100.0	707 15	US-10-440-464-66

14	258	100.0	707	15	US-10-447-315-7	Sequence 7, Appli
15	258	100.0	707	16	US-10-480-621-2	Sequence 2, Appli
16	258	100.0	707	16	US-10-789-241-36	Sequence 36, Appli
17	258	100.0	707	16	US-10-872-198-132	Sequence 132, App
18	258	100.0	707	17	US-10-741-600-1599	Sequence 1599, Ap
19	258	100.0	707	17	US-10-901-417-33	Sequence 33, Appl
20	228	88.4	43	14	US-10-219-329-16	Sequence 16, Appl
21	228	88.4	43	14	US-10-153-185-16	Sequence 16, Appl
22	228	88.4	43	14	US-10-219-561-16	Sequence 16, Appl
23	228	88.4	43	16	US-10-032-376A-16	Sequence 16, Appl
24	228	88.4	43	16	US-10-335-207-16	Sequence 16, Appl
25	150	58.1	171	14	US-10-050-216B-4	Sequence 4, Appli
26	141	54.7	54	14	US-10-219-329-5	Sequence 5, Appli
27	141	54.7	54	14	US-10-153-185-5	Sequence 5, Appli
28	141	54.7	54	14	US-10-219-561-5	Sequence 5, Appli
29	141	54.7	54	16	US-10-032-376A-5	Sequence 5, Appli
30	141	54.7	54	16	US-10-335-207-5	Sequence 5, Appli
31	141	54.7	267	14	US-10-133-797-73	Sequence 73, Appl
32	141	54.7	477	9	US-09-391-104-21	Sequence 21, Appl
33	141	54.7	477	9	US-09-801-196-24	Sequence 24, Appl
34	141	54.7	477	14	US-10-171-311-137	Sequence 137, App
35	141	54.7	477	14	US-10-301-822-127	Sequence 127, App
36	141	54.7	477	14	US-10-131-985-27	Sequence 27, Appl
37	141	54.7	477	15	US-10-295-027-22	Sequence 22, Appl
38	141	54.7	477	15	US-10-115-479-44	Sequence 44, Appl
39	141	54.7	477	15	US-10-211-462-36	Sequence 36, Appl
40	141	54.7	477	15	US-10-447-315-5	Sequence 5, Appli
41	141	54.7	477	17	US-10-901-417-27	Sequence 27, Appl
42	135	52.3	173	15	US-10-115-479-48	Sequence 48, Appl
43	135	52.3	477	15	US-10-115-479-46	Sequence 46, Appl
44	133	51.6	55	14	US-10-219-329-6	Sequence 6, Appli
45	133	51.6	55	14	US-10-153-185-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-219-329-8
; Sequence 8, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Weart, Ilona f.
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443 035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-8

Query Match 100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LKQLSLPFGELDSATLKA...VPLGRFQTPEGLKWHHN 47
Db 1 LKQLSLPFGELDSATLKA...VPLGRFQTPEGLKWHHN 47

RESULT 2

US-10-153-185-8
; Sequence 8, Application US/10153185
; Publication No. US20030148959A1

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-8

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Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 3
US-10-219-561-8
; Sequence 8, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

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Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-032-376A-8
; Sequence 8, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21

; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Homo sapiens
US-10-032-376A-8

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Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 5
US-10-335-207-8
; Sequence 8, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Homo sapiens
US-10-335-207-8

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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

RESULT 6
US-09-391-104-20
; Sequence 20, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-20

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Best Local Similarity 100.0%; Pred. No. 2e-26;
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Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 7

US-09-801-196-36
; Sequence 36, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801.196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
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; SEQ ID NO 36
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-36

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RESULT 8

US-10-171-311-142
; Sequence 142, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yan
; APPLICANT: Schlegel, Robert
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-142

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QY 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 9

US-10-301-822-132
; Sequence 132, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301.822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-132

Query Match 100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 120

RESULT 10

US-10-131-985-33
; Sequence 33, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131.985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 707

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-33

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 11
US-10-295-027-358
; Sequence 358, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Bob Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 358
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1253

Query Match      100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 12
US-10-295-027-1253
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; Sequence 1253, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Bob Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1253

Query Match      100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 13
US-10-440-464-66
; Sequence 66, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
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; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-66

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 14
US-10-447-315-7
; Sequence 7, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1576.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-7

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 15
US-10-480-621-2
; Sequence 2, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupit, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266

; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-2

Query Match 100.0%; Score 258; DB 16; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

Search completed: May 27, 2005, 07:33:59
Job time : 274.564 secs

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A;Molecule type: protein
A;Residues: 20-25,'X',27-37 <VAN>
A;Experimental source: monocytic cell line THP-1
A;Note: sequence extracted from NCBI backbone (NCBIP:G3812) and corrected to correspond
R;Opdenakker, G.; Masure, S.; Grillet, B.; Van Damme, J.
Lymphokine Cytokine Res. 10, 317-324, 1991
A;Title: Cytokine-mediated regulation of human leukocyte gelatinases and role in arthritis
A;Reference number: A61385; MUID:92032113; PMID:1932376
A;Accession: A61385
A;Molecule type: protein
A;Residues: 28-37 <OPD>
R;Masure, S.; Proost, P.; van Damme, J.; Opdenakker, G.
Eur. J. Biochem. 198, 391-398, 1991
A;Title: Purification and identification of 91-kDa neutrophil gelatinase. Release by the
A;Reference number: S16097; MUID:91249834; PMID:1645657
A;Accession: S16097
A;Molecule type: protein
A;Residues: 28-42,'X',44-60,'XX',63 <MAS>
R;Sang, O.X.; Birkedal-Hansen, H.; van Wart, H.E.
Biochim. Biophys. Acta 1251, 99-108, 1995
A;Title: Proteolytic and non-proteolytic activation of human neutrophil progelatinase B.
A;Reference number: S59488; MUID:95399447; PMID:7669817
A;Accession: S59488
A;Molecule type: protein
A;Residues: 20-27;60-67;94-98,'X',100-101;107-114 <SAN>
A;Comment: Gelatinase B hydrolyzes peptide bonds in plasminogen to yield a fragment with
C;Genetics:
A;Gene: GDB:MMP9; CIG4B
A;Cross-references: GDB:125224; OMIM:120361
A;Map position: 20q12-20q13
A;Introns: 46/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 537/2; 584/1; 634/2; 6
C;Function:
A;Description: hydrolyzes type IV collagen
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Product: gelatinase B proenzyme #status predicted <PRE>
F;20-106/Domain: activation peptide #status experimental <PRO>
F;28-707/Product: 91K neutrophil gelatinase B proenzyme #status predicted <PR2>
F;107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>
F;230-271/Domain: fibronectin type II repeat homology <2F9>
F;288-329/Domain: fibronectin type II repeat homology <2F8>
F;347-388/Domain: fibronectin type II repeat homology <2F1>
F;445-497/Domain: proline-rich
F;509-704/Domain: hemopexin repeat homology <PXN>
F;8,120,127/Binding site: carboxylate (Asn) (covalent) #status predicted
F;99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted

Query Match 100.0%; Score 258; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 2
JC4364
N;Alternate names: 92-kDa type IV collagenase; matrix metalloproteinase 9 (MMP9)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4364
R;Okada, A.; Santavica, M.; Basset, P.
Gene 164, 317-321, 1995
A;Title: The cDNA cloning and expression of the gene encoding rat gelatinase B.
A;Reference number: JC4364; MUID:96089602; PMID:7590350
A;Accession: JC4364
A;Molecule type: mRNA
A;Residues: 1-708 <OKA>

A;Cross-references: UNIPROT:P50282; GB:U24441; NID:g1173505; PIDN:AAA90911.1; PID:g1173505
A;Experimental source: skin wounds
C;Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzyme
C;Genetics:
A;Gene: gelB
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-708/Product: progelatinase B #status predicted <PRO>
F;108-708/Product: gelatinase B #status predicted <MAT>
F;214-389/Region: collagen binding #status predicted
F;231-272/Domain: fibronectin type II repeat homology <2F1>
F;289-330/Domain: fibronectin type II repeat homology <2F2>
F;348-389/Domain: fibronectin type II repeat homology <2F3>
F;514-707/Domain: hemopexin repeat homology <PXN>
F;99,121/Binding site: carboxylate (Asn) (covalent) #status predicted
F;100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F;403/Active site: Glu #status predicted
F;519-707/Disulfide bonds: #status predicted

Query Match 91.5%; Score 236; DB 2; Length 708;
Best Local Similarity 87.2%; Pred. No. 1.6e-23;
Matches 41; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
Db 75 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 121

RESULT 3
A53796
Gelatinase B (EC 3.4.24.35) precursor - rabbit
N;Alternate names: 92K matrix metalloproteinase; 92K type IV collagenase; matrix metallo
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A53796; A53398
R;Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Egi
J. Biol. Chem. 269, 15006-15009, 1994
A;Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.
A;Reference number: A53796; MUID:94253056; PMID:8195136
A;Accession: A53796
A;Molecule type: mRNA
A;Residues: 1-707 <EZ>
A;Cross-references: UNIPROT:P41246; GB:D26514; NID:g499372; PIDN:BAA05520.1; PID:g499373
A;Experimental source: osteoclasts
R;Finl, M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Mody, M.K.; Girard, M.T.; Re
J. Biol. Chem. 269, 28620-28628, 1994
A;Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and AP2 in cell
A;Reference number: A53398; MUID:95050662; PMID:7961810
A;Accession: A53398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-75,'p',77-99,'ASR',103-171 <FIN>
A;Cross-references: GB:L36050; NID:9535714; PIDN:AAA64358.1; PID:9535715
C;Genetics:
A;Introns: 46/3; 124/2
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-106/Domain: activation peptide #status predicted <PRO>
F;107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>
F;230-271/Domain: fibronectin type II repeat homology <2F9>
F;288-329/Domain: fibronectin type II repeat homology <2F8>
F;347-388/Domain: fibronectin type II repeat homology <2F1>
F;510-704/Domain: hemopexin repeat homology <PXN>
F;88,120,127/Binding site: carboxylate (Asn) (covalent) #status predicted
F;99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 2.2e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 4
S62507
Gelatinase B (EC 3.4.24.35) precursor - rat
N;Alternate names: collagenase type IV
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62371
R;Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 382, 285-288, 1996
A;Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinant
A;Reference number: S62507; MUID:96184505; PMID:8605986
A;Accession: S62507
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-708 <XIA>
A;Cross-references: UNIPROT:P50282; EMBL:U36476
R;Feng, L.
submitted to the EMBL Data Library, September 1995
A;Reference number: S72371
A;Accession: S72371
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127, 'S', 129-708 <FEN>
A;Cross-references: EMBL:U36476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784
C;Superfamily: Gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-107/Domain: propeptide #status predicted <PRO>
F;25-107/Domain: activation peptide #status predicted <ACT>
F;68-217,393-445/Domain: matrix metalloproteinase homology
F;108-708/Product: gelatinase A #status predicted <MAT>
F;214-389/Region: collagen binding #status predicted
F;231-272/Domain: fibronectin type II repeat homology
F;289-330/Domain: fibronectin type II repeat homology <2F1>
F;348-389/Domain: fibronectin type II repeat homology <2F2>
F;514-707/Domain: hemopexin repeat homology <PXM>
F;100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F;403/Active site: Glu #status predicted
F;519-707/Disulfide bonds: #status predicted

Query Match 90.3%; Score 233; DB 2; Length 708;
Best Local Similarity 85.1%; Pred. No. 4.2e-23;
Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 LQKLSLPQTEGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 121

RESULT 5
I46031
Gelatinase B (EC 3.4.24.35) - bovine
N;Alternate names: matrix metalloproteinase 9 (MMP9)
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46031; S43112
R;Baylis, H.A.; Megson, A.; Hall, R.
Mol. Biochem. Parasitol. 69, 211-222, 1995
A;Title: Infection with *Theileria annulata* induces expression of matrix metalloproteinase
A;Reference number: I46031; MUID:95287902; PMID:7770085
A;Accession: I46031
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-712 <BAY>
A;Cross-references: UNIPROT:P52176; EMBL:X78324; NID:g467620; PIDN:CAAS5127.1; PID:g4676.
A;Note: submitted to the EMBL Data Library, March 1994
C;Genetics:
A;Gene: mmp9
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;67-216,392-444/Domain: matrix metalloproteinase homology #status atypical <MMP>
F;230-271/Domain: fibronectin type II repeat homology <2F1>
F;288-329/Domain: fibronectin type II repeat homology <2F2>
F;347-388/Domain: fibronectin type II repeat homology <2F3>
F;515-709/Domain: hemopexin repeat homology <PXM>
F;99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted

Query Match 87.6%; Score 226; DB 1; Length 712;
Best Local Similarity 84.8%; Pred. No. 3.7e-22;
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 QRLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 6
I52580
gelatinase B (EC 3.4.24.35) precursor - mouse
N;Alternate names: collagenase type IV
C;Species: Mus sp. (mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I52580
R;Graubert, T.; Johnston, J.; Berliner, N.
Blood 82, 3192-3197, 1993
A;Title: Cloning and expression of the cDNA encoding mouse neutrophil gelatinase: demonstration
A;Reference number: I52580; MUID:9403534; PMID:8219207
A;Accession: I52580
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-730 <RES>
A;Cross-references: GB:S67830; NID:g460863; PIDN:AAB28942.1; PID:g460864
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;230-271/Domain: fibronectin type II repeat homology <2F1>
F;288-329/Domain: fibronectin type II repeat homology <2F2>
F;347-388/Domain: fibronectin type II repeat homology <2F3>
F;529-729/Domain: hemopexin repeat homology <PXM>
F;100,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted

Query Match 82.8%; Score 213.5; DB 1; Length 730;
Best Local Similarity 85.1%; Pred. No. 1.8e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 LQKLSLPQTEGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 7
JCI1456
Gelatinase B (EC 3.4.24.35) precursor - mouse
N;Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9 (MMP9)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JCI1456; S39525; I48296; S38654
R;Tanaka, H.; Hojo, K.; Yoshida, H.; Yoshika, T.; Sugita, K.
Biochem. Biophys. Res. Commun. 190, 732-740, 1993
A;Title: Molecular cloning and expression of the mouse 105-kDa gelatinase cDNA.
A;Reference number: JCI1456; MUID:93176173; PMID:8382489
A;Accession: JCI1456
A;Molecule type: mRNA

Figure 1

Db 65 MQKFLGLKMTGKLDSTNTMELMHKRCGVPDVGGSFTFGSPKRWKH 111

RESULT 11

JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse

N:Alternate names: matrix metalloproteinase 10

C:Species: Mus musculus (house mouse)

C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004

C:Accession: JC6505

R:Nadlener, M.; Werner, S.

Gene 202, 75-81, 1997

A:Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).

A:Reference number: JC6505; MUID:98087420; PMID:9427548

A:Accession: JC6505

A:Molecule type: mRNA

A:Residues: 1-476 <NAD>

A:Cross-references: UNIPROT:Q55123; GB:Y13185; NID:G2791311; PIDN:CAA73641.1; PID:G2791311

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C:Genetics:

A:Gene: MMP-10

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase 10

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-476/Product: prostromelysin 2 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:92-218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F:219/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 LQKQLSLPBTGLSDSATLKAMRTPRCGVDPDLGLRFOTFEGDLKW 43

Db 67 MQKFLGLEWTGKLDSTNTMELMHKRCGVPDVGGSFTFGSPKW 109

RESULT 12

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human

N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: A28816; A47496

R:Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988

A:Title: The collagenase gene family in humans consists of at least four members.

A:Reference number: A90339; MUID:88339885; PMID:284164

A:Accession: A28816

A:Molecule type: mRNA

A:Residues: 1-476 <MUL>

A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36629

A:Note: mRNA for this protein was detected in several human tumors

R:Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Boddien, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993

A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene

A:Reference number: A47496; MUID:93352520; PMID:8349617

A:Accession: A47496

A:Molecule type: protein

A:Residues: 17-33 <WIN>

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C:Genetics:

A:Gene: GDB:MMP10; STW2

A:Cross-references: GDB:120392; OMIM:185260

A:Map position: 11q22.3-11q23

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-476/Product: prostromelysin 2 #status experimental <PRO>

F:17-98/Domain: activation peptide #status predicted <ACT>

F:59-263/Domain: matrix metalloproteinase homology <MMP>

F:89-96/Region: autoinhibitory

F:99-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F:119/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted

F:218/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 LQKQLSLPBTGLSDSATLKAMRTPRCGVDPDLGLRFOTFEGDLKW 43

Db 66 MQKFLGLEVTGKLDSTNTMELMHKRCGVPDVGHSFGMPKW 108

RESULT 13

KCRTS2

stromelysin 2 (EC 3.4.24.22) precursor - rat

N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: B26403; A41775; S26498

R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.

Nucleic Acids Res. 15, 1139-1151, 1987

A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A:Reference number: A26403; MUID:871146421; PMID:3547333

A:Accession: B26403

A:Molecule type: mRNA

A:Residues: 1-476 <BRE>

A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57389

A:Note: intron positions were determined by comparison of the cDNA sequence to genomic sequence

R:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; East J. Biol. Chem. 267, 1099-1103, 1992

A:Title: Molecular cloning and characterization of v-mos-activated transformation-associated

A:Reference number: A41775; MUID:92112748; PMID:1370458

A:Accession: A41775

A:Molecule type: mRNA

A:Residues: 1-476 <CHA>

A:Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151

A:Note: sequence extracted from NCBI backbone (NCBIP:76184)

R:de Vouge, M.W.; Mukherjee, B.B.

Oncogene 7, 109-119, 1992

A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of transin

A:Reference number: S26496; MUID:92158347; PMID:1741158

A:Accession: S26498

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 31-103, 'L', 243-242, 'TQMEEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>

A:Cross-references: EMBL:X64020

C:Genetics:

A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-476/Product: prostromelysin 2 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

Db 67 MOKFLGLEMTCKLDSNTMELMHKPRCGVPDVGGFSTFPGSPKW 109

Job time : 18.7756 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 82.25 Seconds
(without alignments)
292.617 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPETGELDSATLKA.....VPLGRFQTPEGLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	707	1 MM09 HUMAN	P14780 homo sapien
2	235	91.1	707	1 MM09 RABIT	P14246 cryctolagus
3	233	90.3	708	1 MM09 RAT	P50282 rattus norv
4	226	87.6	324	2 Q9N282	Q9N282 bos taurus
5	226	87.6	712	1 MM09 BOVIN	P52176 bos taurus
6	216	83.7	149	2 Q9TVB4	Q9TVB4 canis famil
7	216	83.7	704	1 MM09 CANFA	O18733 canis famil
8	216	83.7	704	2 Q71U09	Q71U09 canis famil
9	213.5	82.8	730	1 MM09 MOUSE	P41245 mus musculu
10	213.5	82.8	730	2 Q80X78	Q80X78 mus musculu
11	193	74.8	679	2 Q98856	Q98856 cynops pyrr
12	185	71.7	686	2 Q9DE15	Q9DE15 gallus gall
13	177	68.6	673	2 Q90YB3	Q90YB3 paralicthy
14	176	68.2	671	2 Q6PF33	Q6PF33 xenopus lae
15	176	68.2	671	2 Q9W7L6	Q9W7L6 xenopus lae
16	172	66.7	675	2 Q8QFQ6	Q8QFQ6 oncorhynch
17	170	65.9	674	2 Q98TC6	Q98TC6 cyprinus ca
18	168	65.1	690	2 Q9PVM5	Q9PVM5 oryzias lat
19	167	64.7	670	2 Q6DF16	Q6DF16 xenopus tro
20	160	62.0	680	2 Q7T317	Q7T317 brachydanio
21	141	54.7	477	1 MM03 HUMAN	P08254 homo sapien
22	138	53.5	478	1 MM03 RABIT	P28863 cryctolagus
23	135	52.3	145	2 Q9N283	Q9N283 bos taurus
24	134	51.9	475	1 MM03 RAT	P09238 rattus norv
25	133	51.6	139	2 Q9GM68	Q9GM68 sus scrofa
26	133	51.6	476	1 MM10 HUMAN	P09238 homo sapien
27	133	51.6	476	1 MM10 MOUSE	O55123 mus musculu
28	133	51.6	476	1 MM10 RAT	P07152 rattus norv
29	133	51.6	477	1 MM03 MOUSE	P28862 mus musculu
30	133	51.6	479	2 Q922W6	Q922W6 mus musculu
31	131	50.8	478	2 Q6Y4Q5	Q6Y4Q5 canis famil

RESULT 1

ID	MM09 HUMAN	STANDARD;	PRT;	707 AA.
AC	P14780; Q8N725; Q9H4Z1;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	92 kDa type IV collagenase precursor (SC 3.4.24.35) (92 kDa gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B) (GELB).			
DE	Name=MMP9; Synonyms=CLG4B;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.			
RX	MEDLINE=90008879; PubMed=2551898;			
RA	Wilhelm S.M., Collier I.E., Marmer B.L., Eisen A.Z., Grant G.A., Goldberg G.I.;			
RA	"SV40-transformed human lung fibroblasts secrete a 92-kDa type IV collagenase which is identical to that secreted by normal human macrophages.";			
RT	J. Biol. Chem. 264:17213-17221(1989).			
RJ	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=91358433; PubMed=1653238;			
RX	Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J., Tryggvason K.;			
RA	"Complete structure of the human gene for 92-kDa type IV collagenase. Divergent regulation of expression for the 92- and 72-kilodalton enzyme genes in HT-1080 cells.";			
RT	J. Biol. Chem. 266:16485-16490(1991).			
RJ	[3]			
RN	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RP	Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;			
RA	"SeattlesNPs, NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)";			
RT	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
RJ	[4]			
RN	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RP	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RX	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Babbage A.K., Baggeley C.L., Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			

ALIGNMENTS

32	128	49.6	167	2	Q7ZWD0	Q7ZWD0 brachydanio
33	128	49.6	465	1	MM08 MOUSE	Q70138 mus musculu
34	128	49.6	465	2	Q8C209	Q8C209 mus musculu
35	128	49.6	465	2	Q8C230	Q8C230 mus musculu
36	128	49.6	466	1	MM08 RAT	Q88766 rattus norv
37	128	49.6	475	2	Q71G59	Q71G59 brachydanio
38	127	49.2	393	2	Q8M118	Q8M118 felis silve
39	126	48.8	23	2	Q9UCJ9	Q9UCJ9 homo sapien
40	126	48.8	657	2	Q6DG10	Q6DG10 brachydanio
41	126	48.8	657	2	Q7SZM5	Q7SZM5 brachydanio
42	124	48.1	223	2	Q7TOK9	Q7TOK9 ambystoma m
43	124	48.1	252	2	Q6PWQ3	Q6PWQ3 xenopus lae
44	124	48.1	259	2	Q7ZT19	Q7ZT19 xenopus lae
45	124	48.1	657	2	Q9PTU7	Q9PTU7 oryzias lat

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lencvaslao M.H., Leversha M.A., Lloyd D.M., Lovell J.D.,
 RA Marsh V.D., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=93149601; PubMed=8426746;
 RA Sato H., Seiki M.;
 RT "Regulatory mechanism of 92 kDa type IV collagenase gene expression
 RT which is associated with invasiveness of tumor cells.";
 RL Oncogene 8:395-405 (1993).
 RN [7]
 RP SEQUENCE OF 20-37.
 RX MEDLINE=91355647; PubMed=1653055; DOI=10.1016/1043-4666(91)90021-5;
 RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., van Damme J., Opdenakker G.;
 RT "The cytokine-protease connection: identification of a 96-kD THP-1
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239 (1991).
 RN [8]
 RP SEQUENCE OF 28-60.
 RC TISSUE=Neutrophils;
 RX MEDLINE=91249834; PubMed=1645657;
 RA Masure S., Proost P., van Damme J., Opdenakker G.;
 RT "Purification and identification of 91-kDa neutrophil gelatinase.
 RT Release by the activating peptide interleukin-8.";
 RL Eur. J. Biochem. 198:391-398 (1991).
 RN [9]
 RP CHARACTERIZATION.
 RA Kang K., Lee D.-H.;
 RT "Purification and characterization of human 92-kDa type IV collagenase
 RT (gelatinase B).";
 RL Exp. Mol. Med. 28:161-165 (1996).
 RN [10]
 RP 3D-STRUCTURE MODELING.
 RA Mallena S.C., Sagajkar R.D.;
 RT "Theoretical model of human type IV collagenase precursor.";

RL Submitted (APR-2002) to the PDB data bank.
 RN [11]
 RP VARIANTS VAL-20; LYS-82 AND GLN-279.
 RX MEDLINE=2065865; PubMed=1059806;
 RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.;
 RT "Genetic variation at the matrix metalloproteinase-9 locus on
 RT chromosome 20q12.2-13.1.";
 RL Hum. Genet. 105:418-423 (1999).
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -!- SUBUNIT: Exists as monomer, disulfide-linked homodimer, and as a
 CC heterodimer with a 25 kDa protein. Macrophages and transformed
 CC cell lines produce only the monomeric form.
 CC -!- TISSUE SPECIFICITY: Produced by normal alveolar macrophages and
 CC granulocytes.
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: J05070; AAA51539.1; -;
 DR EMBL: D10051; BAA20967.1; -;
 DR EMBL: AF538844; AM97934.1; -;
 DR EMBL: AL162458; CAC10459.1; -;
 DR EMBL: BC006093; AAH06093.1; -;
 DR FIR: A34458; A34458.
 DR PDB: 1GKC; X-ray; A/B=106-443.
 DR PDB: 1GKD; X-ray; A/B=106-443.
 DR PDB: 1ITV; X-ray; A/B=513-707.
 DR PDB: 1L6J; X-ray; A=20-444.
 DR PDB: 1LKG; Model; A=1-707.
 DR MEROPS: M10.004; -;
 DR GlycoSuiteDB: P14780; -;
 DR Genew: HGNC:7176; MMP9.
 DR H-InvDB: HIX0015874; -;
 DR MIM: 120361; -;
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0008133; F:collagenase activity; TAS.
 DR GO: GO:0008270; F:zinc ion binding; TAS.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR009070; PGSD_like.
 DR InterPro: IPR006970; PT.
 DR Pfam: PF00040; fn2; 3.
 DR Pfam: PF00045; Hemopexin; 4.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS: PR00013; FNTYPEII.
 DR PRINTS: PR00138; MATRXIN.
 DR ProDom: PD000995; FN_Type_II; 2.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Calcium; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19
 FT PROPEP 20 106 Activation peptide.

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FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronectin type-II 1.

Query Match 100.0%; Score 258; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 3.8e-26; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
Db 74 LQKLSLPETGELDSATLKAMTRPCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 2
MM09 RABIT STANDARD; PRT; 707 AA.
AC P4126;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=MMP9;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese white; TISSUE=Bone;
RA MEDLINE=94253056; PubMed=819136;
RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts.";
RL J. Biol. Chem. 269:15006-15009(1994).
RN [2]
RP SEQUENCE OF 1-171 FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=95050662; PubMed=7961810;
RA Fini M.E., Bartlett J.D., Mateubara M., Rinehart W.B., Mody M.K.,
RA Girard M.T., Rainville M.;
RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and
RT AP2 in cell type-specific transcription.";
RL J. Biol. Chem. 269:28620-28628(1994).
CC -I- FUNCTION: Could play a role in bone osteoclastic resorption.
CC -I- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -I- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -I- TISSUE SPECIFICITY: Osteoclasts.
CC -I- SIMILARITY: Belongs to the peptidase M10A family.
CC -I- SIMILARITY: Contains 3 fibronectin type II domains.
CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D26514; BAA05520.1; --
CC EMBL; L36050; AAA64358.1; --
CC PIR; A53796; A53796.
CC HSP; P14780; IGKC.
CC MEROPS; M10.004; --
CC InterPro; IPR000562; FN Type II.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M2n_BS.
CC InterPro; IPR006026; Peptidase_M.
CC InterPro; IPR009070; PGSD_like.
CC InterPro; IPR006970; PT.

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DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF01933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIKIN.
DR PRODOM; PD000995; FN_Type_II; 2.
DR SMART; SM00120; FN; 4.
DR SMART; SM00120; FN; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
- Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 19
FT PROPEP 20 106 Activation peptide (By similarity).
FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronectin type-II 1.
FT DOMAIN 281 339 Fibronectin type-II 2.
FT DOMAIN 340 397 Fibronectin type-II 3.
FT DOMAIN 513 707 Hemopexin-like.
FT SITE 99 99 Cysteine switch (By similarity).
FT METAL 401 401 Zinc (catalytic) (By similarity).
FT ACT_SITE 402 402 Zinc (catalytic).
FT METAL 405 405 Zinc (catalytic) (By similarity).
FT METAL 411 411 Zinc (catalytic) (By similarity).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT DISULFID 516 704 By similarity.
FT CONFLICT 76 76 K -> P (in Ref. 2).
FT CONFLICT 100 102 GVP -> ASR (in Ref. 2).
SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 5.1e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMTRPCGVDPDLGRFQTPEGDLKWHHN 47
    |||||
Db 74 LQKLSLPETGELDSATLKAMTRPCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 3
MM09 RAT STANDARD; PRT; 708 AA.
AC P50282;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=96184505; PubMed=8605986; DOI=10.1016/0014-5793(96)00185-8;
RA Xia Y., Garcia G., Chen S., Wilson C.B., Feng L.;
RT "Cloning of rat 92-kDa type IV collagenase and expression of an active
RT recombinant catalytic domain.";
RL FEBS Lett. 382:285-288(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=96069602; PubMed=7590350; DOI=10.1016/0378-1119(95)00447-E;

```

Okada A., Santavica M., Basset P.;
 "The cDNA cloning and expression of the gene encoding rat gelatinase
 B.",
 Gene 164:317-321(1995).
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 types IV and V.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 DR EMBL; U36476; AB01721.1; -;
 DR EMBL; U24441; AAA90911.1; -;
 DR PIR; JC4364; JC4364.
 DR PIR; S62907; S62907.
 DR HSSP; P14780; 1GKC.
 DR MEROPS; M10.004; -;
 DR RGD; 621320; Mmp9.
 DR InterPro; IPR000562; FN_Type_II; .
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR006970; PT.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR Pfam; PF04886; PT; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM0120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 19 By similarity.
 FT PROPEP 20 107 Activation peptide (By similarity).
 FT CHAIN 108 708 92 kDa type IV collagenase.
 FT DOMAIN 224 281 Fibronectin type-II 1.
 FT DOMAIN 282 340 Fibronectin type-II 2.
 FT DOMAIN 341 398 Fibronectin type-II 3.
 FT DOMAIN 516 708 Hemopexin-like.
 FT SITE 100 100 Cysteine switch (By similarity).
 FT METAL 402 402 Zinc (catalytic) (By similarity).
 FT ACT_SITE 403 403 By similarity.
 FT METAL 406 406 Zinc (catalytic) (By similarity).
 FT METAL 412 412 Zinc (catalytic) (By similarity).
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).
 FT DISULFID 519 707 By similarity.
 FT CONFLICT 2 2 S -> N (in Ref. 2).
 FT CONFLICT 112 112 D -> E (in Ref. 2).
 FT CONFLICT 326 327 AD -> LY (in Ref. 2).
 FT CONFLICT 364 364 S -> G (in Ref. 2).
 FT CONFLICT 441 441 H -> Q (in Ref. 2).
 FT CONFLICT 472 472 S -> P (in Ref. 2).
 FT CONFLICT 515 515 D -> V (in Ref. 2).
 FT CONFLICT 551 551 N -> S (in Ref. 2).

FT CONFLICT 566 566 F -> L (in Ref. 2).
 FT CONFLICT 568 568 S -> A (in Ref. 2).
 FT CONFLICT 579 579 P -> S (in Ref. 2).
 FT CONFLICT 586 589 LWAQ -> SGRK (in Ref. 2).
 FT CONFLICT 597 597 S -> T (in Ref. 2).
 FT CONFLICT 669 669 Q -> H (in Ref. 2).
 SQ SEQUENCE 708 AA; 78610 MW; D57DC0D1B93A778C CRC64;
 Query Match 90.3%; Score 233; DB 1; Length 708;
 Best Local Similarity 85.1%; Pred. No. 9.6e-23;
 Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKQLSLPTGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 DB 75 LKQLSLPTGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 121
 RESULT 4
 Q9N282 PRELIMINARY; PRT; 324 AA.
 AC Q9N282;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE MWP-9 (Fragment).
 GN Name-bmmp-9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RA Sato T., Hirata M., Ito A., Hashizume K.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB043996; BAA96389.1; -;
 DR HSSP; P14780; 1GKD.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR009070; PGSD_like.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00059; FN2_2.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 36273 MW; 4137C9820C28B080 CRC64;
 Query Match 87.6%; Score 226; DB 2; Length 324;
 Best Local Similarity 84.8%; Pred. No. 3.5e-22;
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 QKQLSLPTGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 DB 75 QKQLSLPTGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 120
 RESULT 5
 MM09 BOVIN STANDARD; PRT; 712 AA.
 ID MM09 BOVIN
 AC P52176;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa

DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN Name=MMP9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RA MEDLINE=55287902; PubMed=7770085; DOI=10.1016/0166-6851(94)00216-A;
 RX Baylis H.A., Megson A., Hall R.;
 RT "Infection with Theileria annulata induces expression of matrix
 RT metalloproteinase 9 and transcription factor AP-1 in bovine
 RT leucocytes.";
 RL Mol. Biochem. Parasitol. 69:211-222(1995).
 CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
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 CC -----
 DR EMBL: X78324; CA55127.1; -;
 DR PIR: I46031; I46031.
 DR HSSP: P14780; IGD.
 DR MEROPS: M10.004; -;
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR006026; Peptidase_M.
 DR InterPro: IPR009070; PGBD_like.
 DR InterPro: IPR006970; PT.
 DR Pfam: PF00040; fn2; 3.
 DR Pfam: PF00045; Hemopexin; 4.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS: PR00013; FNTYPEII.
 DR PRINTS: PR00138; MATRINX.
 DR ProDom: PD000995; FN_Type_II; 2.
 DR SMART: SM00059; FN2; 3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZnMc; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00024; HEMOPEXIN; FALSE_NEG.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metalloproteinase; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 19
 FT CHAIN 107 712
 FT DOMAIN 223 280
 FT DOMAIN 281 339
 FT DOMAIN 340 397
 FT DOMAIN 518 712
 FT SITE 99 99
 FT METAL 401 401
 FT ACT_SITE 402 402
 FT METAL 405 405
 FT METAL 411 411
 zinc (catalytic) (By similarity).
 zinc (catalytic) (By similarity).
 zinc (catalytic) (By similarity).

FT DISULFID 521 709 By similarity.
 FT CARBOHYD 38 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 712 AA; 79087 MW; E7FDA28372AEEOCE CRC64;
 Query Match 87.6%; Score 226; DB 1; Length 712;
 Best Local Similarity 84.8%; Pred. No. 8.7e-22;
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 QKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 75 QRRSLPETGELDSTTLNAMRAPRCGVDPDVGRTFEGELKWHHN 120
 RESULT 6
 Q9TVB4 PRELIMINARY; PRT; 149 AA.
 ID Q9TVB4
 AC Q9TVB4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Type IV collagenase MMP-9 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibrosarcoma;
 RA Bittner B.C., Kitchell B.E.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF147104; AAD31323.1; -;
 DR HSSP: P14780; IGD.
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR009070; PGBD_like.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR PRINTS: PR00138; MATRINX.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR COLLAGEN.
 DR NON_TER 149 149
 SQ SEQUENCE 149 AA; 17025 MW; CA6A5062EFDCCBBF CRC64;
 Query Match 83.7%; Score 216; DB 2; Length 149;
 Best Local Similarity 78.7%; Pred. No. 3.2e-21;
 Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQRRLLPETGELDKTTLEAMRAPRCGVDPDLGRFQTFEGDLKWHND 120
 RESULT 7
 MM09 CANFA STANDARD; PRT; 704 AA.
 ID MM09 CANFA
 AC O18733; O19130;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN Name=MMP9;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE (GELB)) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB)
 GN Names=Mmp9; Synonyms=C194b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=941179406; PubMed=8137709; DOI=10.1083/jcb.124.6.1091;
 RA Reponen P., Sahlberg C., Munaut C., Theleff I., Tryggvason K.;
 RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
 RT osteoclast lineage during mouse development.";
 RT J. Cell Biol. 124:1091-1102(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=931176173; PubMed=8382489;
 RA Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
 RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
 RT cDNA.";
 RT Biochem. Biophys. Res. Commun. 190:732-740(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=94062823; PubMed=8243459;
 RA Masure S., Nys G., Fiten P., van Damme J., Opdenakker G.;
 RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
 RT glycosylation in WH1-3 macrophages and gene organisation.";
 RT Eur. J. Biochem. 218:129-141(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94033534; PubMed=8219207;
 RA Graubert T., Johnston J., Berliner N.;
 RT "Cloning and expression of the cDNA encoding mouse neutrophil
 RT gelatinase: demonstration of coordinate secondary granule protein gene
 RT expression during terminal neutrophil maturation.";
 RT Blood 82:3192-3197(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Sato R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gianni C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z27231; CAA81745.1; -;
 CC EMBL; D12712; BAA02208.1; -;
 CC EMBL; X72794; CAA51314.1; -;
 CC EMBL; X72795; CAA51315.1; -;
 CC EMBL; S67830; AAB28942.1; -;
 CC EMBL; AK004651; BAB23442.1; -;
 CC F1R; JCI456; JCI456.
 CC HSSP; P14780; 1GKC.
 CC MEROPS; M10.004; -;
 CC MGD; MG1:97011; Mmp9.
 CC InterPro; IPR000562; FN_Type_II.
 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR001818; Pept_M10A_M12B.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR006026; Peptidase_M.
 CC InterPro; IPR009070; PGED_like.
 CC InterPro; IPR009070; PT.
 CC Pfam; PF00040; fn2; 3.
 CC Pfam; PF00045; Hemopexin; 4.
 CC Pfam; PF00413; Peptidase_M10; 1.
 CC Pfam; PF03933; Peptidase_M10_N; 1.
 CC Pfam; PF04886; PT; 2.
 CC PRINTS; PR00013; FNTYPEII.
 CC PRINTS; PR00138; MATRXIN.
 CC ProDom; PD000995; FN_Type_II; 2.
 CC SMART; SM00059; FN2; 3.
 CC SMART; SM00120; HX; 4.
 CC SMART; SM00235; ZnMc; 1.
 CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE; PS00023; FIBRONECTIN_2; 3.
 CC PROSITE; PS00024; HEMOPEXIN; 1.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 CC Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;
 CC Zymogen.
 KW SIGNAL 1 19 By similarity.
 FT PROPEP 20 107 Activation peptide (By similarity).
 FT CHAIN 108 730 92 kDa type IV collagenase.
 FT DOMAIN 223 280 Fibronectin type-II 1.
 FT DOMAIN 281 339 Fibronectin type-II 2.
 FT DOMAIN 340 397 Fibronectin type-II 3.
 FT DOMAIN 531 730 Hemopexin-like.
 FT SITE 100 100 Cysteine switch (By similarity).
 FT METAL 401 401 Zinc (catalytic) (By similarity).
 FT ACT_SITE 402 402 Zinc (catalytic).
 FT METAL 411 411 Zinc (catalytic) (By similarity).
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 FT DISULFID 534 729 By similarity.
 FT VARIANT 514 514 A -> P.
 FT VARIANT 639 639 P -> L.
 FT VARIANT 711 711 P -> H.
 FT CONFLICT 20 20 A -> C (in Ref. 4).
 FT CONFLICT 25 26 QP -> HA (in Ref. 4).

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FT CONFLICT 466 466 P -> T (in Ref. 5).
FT CONFLICT 514 514 A -> P (in Ref. 5).
FT CONFLICT 639 639 P -> L (in Ref. 5).
FT CONFLICT 711 711 P -> H (in Ref. 5).
SQ SEQUENCE 730 AA; 80453 MW; E1911F6D5CCAC059 CRC64;

Query Match 82.8%; Score 213.5; DB 1; Length 730;
Best Local Similarity 85.1%; Pred. No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
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Db 75 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 10
Q80X18 PRELIMINARY; PRT; 730 AA.
AC Q80X18;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase 9.
GN Name=Mmp9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Arnason R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC046991; AAH46991.1; -.
DR HSSP; P14780; 1GKC.
DR MGD; MGI:97011; Mmp9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004222; F:metalloendopeptidase activity; IDA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR InterPro; IPR006970; PT.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 75 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

Query Match 82.8%; Score 213.5; DB 2; Length 730;
Best Local Similarity 85.1%; Pred. No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
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Db 75 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 11
Q98856 PRELIMINARY; PRT; 679 AA.
ID Q98856;
AC Q98856;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902; DOI=10.1073/pnas.93.13.6819;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
DR EMBL; D82052; BAAL1523.1; -.
DR HSSP; P08253; 1J7M.
DR MEROPS; M10.004; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTPEI1.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
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DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 730 AA; 80535 MW; E16F45C24D4D1024 CRC64;

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Best Local Similarity 85.1%; Pred. No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

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RESULT 11
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ID Q98856;
AC Q98856;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902; DOI=10.1073/pnas.93.13.6819;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
DR EMBL; D82052; BAAL1523.1; -.
DR HSSP; P08253; 1J7M.
DR MEROPS; M10.004; -.
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DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTPEI1.
DR PRINTS; PR00138; MATRXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
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DR PROSITE; PS00024; HEMOPEXIN; 1.
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DR EMBL; AF072455; AD41624.1; -.
DR HSPR; P33435; 1CXV.
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DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_I1.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
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DR Pfam; PF00045; Hemopexin; 4.
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DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZNMC; 1.
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DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
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Job time : 85.25 secs
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 26.3077 Seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	292	100.0	469	3	US-08-448-489-12
3	292	100.0	469	3	US-09-521-220-16
4	292	100.0	469	3	US-09-391-104-23
5	292	100.0	469	4	US-09-949-016-6223
6	292	100.0	469	4	US-09-689-730-12
7	292	100.0	431	4	US-09-949-016-10875
8	214	73.3	444	1	US-09-178-002-2
9	214	73.3	466	3	US-08-704-711A-17
10	214	73.3	466	3	US-09-521-220-17
11	214	73.3	467	1	US-09-178-002-4
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14	214	73.3	468	4	US-09-689-730-13
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17	189	64.7	476	3	US-09-521-220-21
18	189	64.7	476	3	US-09-391-104-22
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20	189	64.7	476	4	US-09-689-730-14
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23	189	64.7	477	3	US-08-281-313-1
24	189	64.7	477	3	US-09-521-220-20
25	189	64.7	477	3	US-09-391-104-21
26	189	64.7	477	4	US-09-689-730-15
27	189	64.7	484	4	US-09-949-016-10877

28	163	55.8	471	3	US-09-391-104-25	Sequence 25, Appl
29	163	55.8	480	4	US-09-949-016-10560	Sequence 10560, A
30	163	55.8	513	4	US-09-862-631-4	Sequence 4, Appl
31	159	54.5	470	3	US-08-068-392-2	Sequence 2, Appl
32	159	54.5	470	3	US-08-396-988-2	Sequence 2, Appl
33	159	54.5	470	3	US-09-391-104-26	Sequence 28, Appl
34	159	54.5	473	4	US-09-949-016-10876	Sequence 10876, A
35	158	54.1	663	4	US-09-194-468A-30	Sequence 30, Appl
36	154	52.7	471	4	US-08-994-689C-1	Sequence 1, Appl
37	151	51.7	264	3	US-09-009-156-6	Sequence 6, Appl
38	151	51.7	264	3	US-09-372-154-6	Sequence 6, Appl
39	151	51.7	267	3	US-08-448-489-18	Sequence 18, Appl
40	151	51.7	267	3	US-09-391-104-27	Sequence 27, Appl
41	151	51.7	267	3	US-09-689-730-18	Sequence 18, Appl
42	151	51.7	271	3	US-08-896-062-2	Sequence 2, Appl
43	151	51.7	277	4	US-09-949-016-8131	Sequence 8131, Ap
44	150	51.4	135	4	US-09-513-999C-4163	Sequence 4163, Ap
45	147	50.3	471	4	US-08-994-689C-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horet
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-16

Query Match 100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
DB 67 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 2

US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match 100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
DB 67 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 3

US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>

; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

; INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

Query Match 100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
DB 67 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 4

US-09-391-104-23
; Sequence 23, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match 100.0%; Score 292; DB 3; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
DB 67 MOEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||

RESULT 5

US-09-949-016-6223
; Sequence 6223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6223
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6223

Query Match      100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 6
US-09-689-730-12
; Sequence 12, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-250P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-12

Query Match      100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 7
US-09-949-016-10875
; Sequence 10875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10875
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10875

Query Match      100.0%; Score 292; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 54
Db 89 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 142

RESULT 8
US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match      73.3%; Score 214; DB 1; Length 444;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVDAQFVLTEGPNRWEQTHLYRIEN 54
Db 43 MQEFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRN 96

RESULT 9
US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA: WO PCT/DE95/00357
; APPLICATION NUMBER: 17-MAR-1995
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLYRIEN 119

RESULT 10
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILLI, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17

Query Match 73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLYRIEN 119

RESULT 11
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLYRIEN 119

RESULT 12
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-24

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 20.4231 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDALTKV.....VLTEGNRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	468	1 KCHUI	interstitial colla
3	270	92.5	489	1 KCPGI	interstitial colla
4	234	80.1	469	1 KCB01	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase (EC 3.1.1.1)
6	214	73.3	467	1 KCHUN	neutrophil colla
7	189	64.7	476	1 KCHUS2	stromelysin 2 (EC 3.4.21.1)
8	189	64.7	477	1 KCHUS1	stromelysin 1 (EC 3.4.21.1)
9	186	63.7	478	1 KCHRS1	stromelysin 1 (EC 3.4.21.1)
10	173	59.2	476	1 JC6505	stromelysin 2 (EC 3.4.21.1)
11	173	59.2	477	1 KCM5S1	stromelysin 1 (EC 3.4.21.1)
12	172	58.9	475	1 KCRTHI	stromelysin 1 (EC 3.4.21.1)
13	172	58.9	483	2 JC5743	matrix metallopro
14	168	57.5	472	2 S29243	interstitial colla
15	167	57.2	476	1 KCRS2	stromelysin 2 (EC 3.4.21.1)
16	163	55.8	471	2 A53711	collagenase 3 (EC 3.4.21.1)
17	162	55.5	466	2 A23685	interstitial colla
18	159	54.5	470	2 A49499	gelatinase HM
19	158	54.1	663	1 S46492	gelatinase A (EC 3.4.21.1)
20	155	53.1	267	2 A57490	matrilysin (EC 3.4.21.1)
21	151	51.7	267	1 KCHUM	matrilysin (EC 3.4.21.1)
22	146	50.0	662	2 S70365	gelatinase A (EC 3.4.21.1)
23	144	49.3	462	2 A42401	macrophage elastase
24	144	49.3	660	1 A28153	gelatinase A (EC 3.4.21.1)
25	144	49.3	662	2 A42496	gelatinase A (EC 3.4.21.1)
26	144	49.3	662	2 S34780	gelatinase A (EC 3.4.21.1)
27	135	46.2	708	2 S62307	gelatinase B (EC 3.4.21.1)
28	134.5	46.1	582	2 I38028	matrix metallopro
29	133	45.5	708	2 JC4364	gelatinase B (EC 3.4.21.1)

ALIGNMENTS

RESULT 1

KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human

N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col

C/Species: Homo sapiens (man)

C/Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C/Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S53

R/Template: N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-Stev

Cancer Res. 50, 5431-5437, 1990

A/Title: Cloning and characterization of human tumor cell interstitial collagenase.

A/Reference number: A37308; MUID:90352587; PMID:2167156

A/Accession: A37308

A/Molecule type: mRNA

A/Residues: 1-469 <TEM>

A/Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126

R/Brinckhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.

J. Clin. Invest. 79, 542-546, 1987

A/Title: Molecular cloning of human synovial cell collagenase and selection of a single

A/Reference number: S22766; MUID:87109799; PMID:3027129

A/Accession: S22766

A/Molecule type: DNA

A/Residues: 1-63,65-70 <BRI>

A/Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667

R/Angel, P.; Baumann, I.; Stein, B.; Delius, H.; Rahmsdorf, H.J.; Herrlich, P.

Mol. Cell. Biol. 7, 2256-2266, 1987

A/Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene

A/Reference number: I57620; MUID:87257941; PMID:3037355

A/Accession: I57620

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-35 <RES>

A/Cross-references: GB:M16567; NID:G180668; PIDN:AAA52033.1; PID:G180669

R/Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.

J. Biol. Chem. 261, 6600-6605, 1986

A/Title: Human fibroblast collagenase. Complete primary structure and homology to an onc

A/Reference number: A00996; MUID:86196089; PMID:3009463

A/Accession: A00996

A/Molecule type: mRNA

A/Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>

A/Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665

A/Note: part of this sequence was confirmed by protein sequencing of the proenzyme

R/Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A/Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis

A/Reference number: A90336; MUID:87156645; PMID:3030290

A/Accession: D29157

A/Molecule type: mRNA

A/Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>

A/Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA28858.1; PID:G38267

A/Note: parts of this sequence, including the amino end of the proenzyme and of the matu

R/Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Brown, A.S.; Birkedal-Hansen, H.

Biochemistry 27, 6751-6758, 1988

gelatinase B (EC 3.4.21.1)
gelatinase B (EC 3.4.21.1)
matrix metallopro
matrix metallopro
gelatinase B (EC 3.4.21.1)
pro-matrix metallo
gelatinase B (EC 3.4.21.1)
gelatinase B (EC 3.4.21.1)
matrix metallopro
probable metallopr
metalloproteinase
probable metallopr
probable metallopr
probable matrix me
hypochemical prote
probable matrix me

707 1 A34458
707 1 A53796
582 2 I84471
689 2 I38029
712 1 I46031
82 2 PW0052
730 1 I52580
730 2 JCI456
582 2 I48673
364 2 E71433
341 2 T51957
342 2 G84885
305 2 T08836
579 2 T37248
598 2 T32166
521 2 T37252

30 132 45.2
31 130 44.5
32 126.5 43.3
33 126.5 43.3
34 126 43.2
35 124 42.5
36 120.5 41.3
37 120.5 41.3
38 118.5 40.6
39 111 38.0
40 108 37.0
41 108 37.0
42 106.5 36.5
43 103.5 35.4
44 103.5 35.4
45 100 34.2

A;Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzymatic end of the activated enzyme. PMID:2461732
A;Reference number: A44518; MUID:89062403; PMID:2461732
A;Accession: A44518
A;Molecule type: protein
A;Residues: 270-305 <BIR>
R;Clark, I.M.; Cawston, T.E.
Biochem. J. 263, 201-206, 1989
A;Title: Fragments of human fibroblast collagenase. Purification and characterization.
A;Reference number: S06132; MUID:90104231; PMID:2557822
A;Accession: S06132
A;Status: preliminary
A;Molecule type: protein
A;Residues: 100-102,'P',104-107,'XX',110-112;270-277,'X',279-280,'X',282-287 <CLA>
R;Lark, M.W.; Walakowits, L.A.; Shah, T.K.; Vamiddleworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta stimulated cells. PMID:2173990
A;Reference number: A60964; MUID:91059606; PMID:2173990
A;Accession: B60964
A;Molecule type: protein
A;Residues: 24-35;100-108;270-272,'X',274,'X',276 <LAR>
R;Suzuki, K.; Nagase, H.; Ito, A.; Enghild, J.J.; Salvesen, G.
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990
A;Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rheumatoid synovial cells. PMID:2169257
A;Reference number: S10595; MUID:90380300; PMID:2169257
A;Accession: S10595
A;Molecule type: protein
A;Residues: 20-102 <SU2>
R;Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.
Biochem. J. 305, 301-306, 1995
A;Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collagenase) and 3 (matrilysin) by tissue inhibitors of metalloproteinases (TIMPs).
A;Reference number: S53438; MUID:95126921; PMID:7826345
A;Accession: S53438
A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-108 <SU2>
R;Springman, E.B.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A;Title: Multiple modes of activation of latent human fibroblast collagenase: evidence for a role for tissue inhibitors of metalloproteinases (TIMPs).
A;Reference number: A44517; MUID:90115877; PMID:2153297
A;Contents: annotation; disulfide bond; activation mechanism
R;Salowe, S.P.; Marcy, A.I.; Cuca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes
Biochemistry 31, 4535-4540, 1992
A;Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry of zinc binding and effect of zinc on the catalytic activity. PMID:1581308
A;Reference number: A4303; MUID:92256384; PMID:1581308
A;Contents: annotation; zinc ligand in proenzyme
A;Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the catalytic site are activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase can be activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.
C;Genetics:
A;Gene: GDB:MMP1; CUG
A;Cross-references: GDB:119783; OMIM:120353
A;Map position: 11q22.2-11q22.3
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C-supernatant; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-469/Product: procollagenase #status experimental <PRO>
F;20-99/Domain: activation peptide #status experimental <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status experimental <MAT>
F;92-466/Domain: hemopexin repeat homology <PXN>
F;92-218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;269-270/Disulfide bonds: Pro-Ile (autolytic) #status experimental
F;278-466/Disulfide bonds: #status experimental

Query Match 100.0%; Score 292; DB 1; Length 469;

Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFGKLVGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 67 MQEFGKLVGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||
RESULT 2
KCRBI
Interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase; Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A27500; B27500; I46694
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloproteinases.
A;Reference number: A27500; MUID:88077876; PMID:2825772
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <PIN>
A;Cross-references: UNIPROT:P13943; GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391;399-468 <PI2>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerhoff, C.E.; Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial cell collagenase and human fibroblast collagenase.
A;Reference number: I46694; MUID:87029174; PMID:3021384
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <PI3>
A;Cross-references: GB:M25663; NID:9531211; PID:AAA31203.1; PID:9531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the activation peptide by other proteinases.
C;Comment: Procollagenase can be activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.
C;Genetics:
A;Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
A;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C-supernatant; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-468/Product: procollagenase #status predicted <PRO>
F;19-98/Domain: activation peptide #status predicted <ACT>
F;59-260/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;119,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

Query Match 96.9%; Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 3.6e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQEFGKLVGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
|||||
Db 66 MQEFGKLVGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 119
|||||

RESULT 3

KCPGI

Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase

C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S15986; MUID:91333421; PMID:1651440
 R;Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
 Matrix 11, 161-167, 1991
 A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
 A;Reference number: S15986; MUID:91333421; PMID:1651440
 A;Accession: S15986
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-469 <RIC>
 A;Cross-references: UNIPROT:P11692
 A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
 R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
 Nucleic Acids Res. 18, 6703, 1990
 A;Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
 A;Reference number: S13597; MUID:91067477; PMID:2174547
 A;Accession: S13597
 A;Molecule type: mRNA
 A;Residues: 25-469 <CLA>
 A;Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269
 R;Li, J.; Brick, P.; Blow, D.M.
 submitted to the Brookhaven Protein Data Bank, April 1995
 A;Reference number: A65568; PDB:1FBL
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
 C;Comment: Procollagenase can be activated without removal of the activation peptide. St
 tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
 C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
 A;Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-469/Product: procollagenase #status predicted <PRO>
 F;20-99/Domain: activation peptide #status experimental <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PKN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;
 Best Local Similarity 90.7%; Pred. No. 1.5e-25;
 Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54
 Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTPGNPRWENTHLYTRYEN 120

RESULT 4
 KCBOI
 N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
 C;Species: *Bos primigenius taurus* (cattle)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S14654; S20336; S14655
 R;Tamura, M.; Shimokawa, H.; Sasaki, S.
 submitted to the EMBL Data Library, March 1991
 A;Reference number: S14654
 A;Accession: S14654
 A;Molecule type: mRNA
 A;Residues: 1-469 <TAM>
 A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260
 R;Sudbeck, B.D.; Jeffrey, J.J.; Weigun, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
 Arch. Biochem. Biophys. 293, 370-376, 1992
 A;Title: Purification and characterization of bovine interstitial collagenase and tissue
 A;Reference number: S20336; MUID:92161820; PMID:1311165
 A;Accession: S20336

A;Molecule type: protein
 A;Residues: 19-21, 'EP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125 <F
 C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
 C;Comment: Procollagenase can be activated without removal of the activation peptide. St
 tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
 C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-469/Product: procollagenase #status predicted <PRO>
 F;19-99/Domain: activation peptide #status predicted <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;90-97/Region: autoinhibitory
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PKN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;
 Best Local Similarity 81.5%; Pred. No. 4.2e-21;
 Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54
 Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTPGKSCWENTHLYTRYEN 120

RESULT 5
 I51267
 collagenase (EC 3.4.24.-) - bullfrog
 C;Species: *Rana catesbeiana* (bullfrog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51267
 R;Oofusa, K.; Yomori, S.; Yoshizato, K.
 Int. J. Dev. Biol. 38, 345-350, 1994
 A;Title: Regionally and hormonally regulated expression of genes of collagen and collag
 A;Reference number: I51267; MUID:95071832; PMID:7981043
 A;Accession: I51267
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-384 <OOF>
 A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:g913070; PIDN:AAB32661.1; PID:g913071
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;53-231/Domain: matrix metalloproteinase homology <MMP>
 F;236-381/Domain: hemopexin repeat homology <PKN>
 F;81,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
 F;190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;
 Best Local Similarity 79.6%; Pred. No. 6.9e-21;
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54
 Db 57 LKQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTPGNPRWENTHLYTRYEN 109

RESULT 6
 KCHUN
 N;Alternate names: matrix metalloproteinase 8
 C;Species: *Homo sapiens* (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A37073; A61175; A3230; S09680; S11026; S19576; S27225; S32527; S624
 R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.F.; Spinella, D.G.; Stever
 J. Biol. Chem. 265, 11421-11424, 1990

A;Title: Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.
 A;Reference number: A37073; MUID:90307647; PMID:2164002
 A;Accession: A37073
 A;Molecule type: mRNA
 A;Residues: 1-467 <HAS>
 A;Cross-references: UNIPROT:P22894; GB:J05556; NID:g180618
 R;Devavajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
 Blood 77, 2731-2738, 1991
 A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
 A;Reference number: A61175; MUID:91255696; PMID:1646048
 A;Accession: A61175
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-31,'I',33-86,'E',88-467 <DEV>
 A;Accession: B61175
 A;Molecule type: protein
 A;Residues: 263-264,'X',266-270,'X',272-273,'X',275,'X',277 <DE>
 R;Wallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V Biochemistry 29, 10628-10634, 1990
 A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with other members of the matrix metalloproteinase family.
 A;Reference number: A36230; MUID:91104978; PMID:2176876
 A;Accession: A36230
 A;Molecule type: protein
 A;Residues: 'X',86-87,'X',89-90,'X',92-97,'X',99-111,'X',113-120 <MAL>
 R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
 Eur. J. Biochem. 189, 295-300, 1990
 A;Title: Characterization and activation of procollagenase from human polymorphonuclear neutrophils.
 A;Reference number: S09680; MUID:90249372; PMID:2159879
 A;Accession: S09680
 A;Molecule type: protein
 A;Residues: 21-31,'I',33-39,'I',41-47,'V',49-53,'I',55-72,'G',74-86,'E',88-111,'X',113-114
 A;Note: 67-Lys was also found
 R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
 Biol. Chem. Hoppe-Seyler 371, 733, 1990
 A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.
 A;Reference number: S11026; MUID:91000455; PMID:2169766
 A;Note: original publication was Biol. Chem. Hoppe-Seyler 371(Suppl.), 295-304, 1990
 A;Accession: S11026
 A;Molecule type: protein
 A;Residues: 21-31,'I',33-53,'I',55-72,'G',74-111,'X',113-140,183-203,'X',205-209,248-261
 A;Note: 87-Glu was also found
 R;Blaeser, J.; Knaeuper, V.; Osthuus, A.; Reinke, H.; Tschesche, H.
 Eur. J. Biochem. 202, 1223-1230, 1991
 A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
 A;Reference number: S19576; MUID:92111500; PMID:1662606
 A;Accession: S19576
 A;Molecule type: protein
 A;Residues: 69-103 <BL2>
 R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.
 FEBS Lett. 313, 59-61, 1992
 A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.
 A;Reference number: S27225; MUID:93050220; PMID:1330697
 A;Accession: S27225
 A;Molecule type: protein
 A;Residues: 68-103 <BLA>
 R;Knaeuper, V.; Osthuus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.
 Biochem. J. 291, 847-854, 1993
 A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
 A;Reference number: S32527; MUID:93256897; PMID:8489511
 A;Accession: S32527
 A;Molecule type: protein
 A;Residues: 100-112;263-276 <KN3>
 R;Knaeuper, V.; Murphy, G.; Tschesche, H.
 Eur. J. Biochem. 235, 187-191, 1996
 A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
 A;Reference number: S62608; MUID:96202934; PMID:8631328
 A;Accession: S62608
 A;Molecule type: protein
 A;Residues: 21-39,'I',41-47,'V',49-122 <KN4>
 R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
 submitted to the Brookhaven Protein Data Bank, January 1994
 A;Reference number: A67078; PDB:1MNC
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G',106-149,'G',1

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahli, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, J. Nat. Struct. Biol. 1, 119-123, 1994
 A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.
 A;Reference number: A58274; MUID:95384762; PMID:7656015
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G',106-149,'G',149-150
 C;Comment: This protein is more highly glycosylated than interstitial collagenase and is a member of the matrix metalloproteinase family.
 C;Genetics:
 A;Gene: GDB:MWP8; CIG1
 A;Cross-references: GDB:128173; OMIM:120355
 A;Map position: 11q22.2-11q22.3
 C;Function:
 A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous tissues.
 A;Note: cleaves type I collagen most rapidly
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; ne F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-467/Product: procollagenase #status predicted <PRO>
 F;21-100/Domain: activation peptide #status experimental <ACT>
 F;59-262/Domain: matrix metalloproteinase homology <MWP>
 F;89-96/Region: autoinhibitory
 F;101-467/Product: neutrophil collagenase #status predicted <MAT>
 F;273-464/Domain: hemopexin repeat homology <BXN>
 F;54,73,112,119,204,246/Binding site: carboxydrate (Asn) (covalent) #status predicted
 F;73-74/Cleavage site: Asp-Val (autolytic) #status experimental
 F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental
 F;91-217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status experimental
 F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental
 F;167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His, His) #status experimental
 F;174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status experimental
 F;217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental
 F;218/Active site: Glu #status predicted
 F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental
 F;279-464/Disulfide bonds: #status predicted
 Query Match 73.3%; Score 214; DB 1; Length 467;
 Best Local Similarity 70.4%; Pred. No. 1.2e-18;
 Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 OY 1 MQEFGKLVGTPDQETLKVKKQPCGVPDVAQFVLTEGNPRWEQTHLTYYRIN 54
 DB 66 MORFFGLNVGTPNEETLDMKKKPCGVPDGGFMLTPGNPKWERTNLTYYRIN 119
 RESULT 7
 KCHUS2
 Stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
 N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A28816; A47496
 R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, P. Biochem. J. 253, 187-192, 1988
 A;Title: The collagenase gene family in humans consists of at least four members.
 A;Reference number: A30339; MUID:88339885; PMID:2844164
 A;Accession: A28816
 A;Molecule type: mRNA
 A;Residues: 1-476 <MUI>
 A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:g36628; PIDN:CAA30679.1; PID:g36629
 A;Note: mRNA for this protein was detected in several human tumors
 R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993
 A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene.
 A;Reference number: A47496; MUID:93352520; PMID:8349617
 A;Accession: A47496
 A;Molecule type: protein
 A;Residues: 17-33 <WIN>
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
 C;Genetics:
 A;Gene: GDB:MMPI0; STMY2
 A;Cross-references: GDB:120392; OMIM:185260
 A;Map position: 11q22.3-11q23
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

Biochemistry 37, 4699-4702, 1998
A>Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (MMP3)
A:Reference number: A58812; MUID:9548733; PMID:9548733
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February 1997
A:Reference number: A58466; PDB:1HRS
A:Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160
F:Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D. Protein Sci. 4, 1966-1976, 1995
A>Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain an
A:Reference number: A58814; MUID:96117647; PMID:9535233
A:Contents: annotation; X-ray crystallography, 1.70 angstroms
F:Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K. Biochemistry 30, 6476-6483, 1991
A>Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch
A:Reference number: A39589; MUID:91274298; PMID:1647201
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1995
A:Reference number: A56637; PDB:1SLM
A:Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47;57-267
R:Gooley, P.R.; O'Connell, J.F.
submitted to the Brookhaven Protein Data Bank, March 1995
A:Reference number: A67284; PDB:2SRT
A:Contents: annotation; conformation by (1)H-NMR, residues 100-272
R:Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Esser Biochemistry 32, 13098-14008, 1993
A>Title: Secondary structure and zinc ligation of human recombinant short-form stromelysin;
A:Reference number: A58815; MUID:94059987; PMID:8241164
A:Contents: annotation; confirmation by (1)H-NMR
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation site.
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of which are active.
C:Genetics:
A:Gene: GDB:MMP3; STMY; STMV1
A:Cross-references: GDB:I20727; OMIM:185250
A:Map position: 11q23-11q23
C:Function:
A>Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side of aspartate or glutamate residues.
A>Note: degrades various extracellular matrix proteins, including fibronection, plasminogen C superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinases; calcium; extracellular matrix; fibronectin; hyaluronan; proteoglycan; laminin F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-47/Product: prostomelysin 1 #status experimental <PRO>
F:18-99/Domain: activation peptide #status experimental <ACT>
E:60-264/Domain: matrix metalloprotease homology <MMP>
F:100-477/Product: stromelysin 1 #status experimental <MAT>
F:284-477/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (cys, his, His) (inhibited) #status experimental
F:120/Binding site: carbohydrate (asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (his) (active) #status experimental
F:219/Active site: Glu #status predicted
F:290-477/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred No. 1.6e-15;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 1 MQEFFGLKVTGKDPAETLKVMMQPCGVDPDVAQAFLTEGNPRWEQTHLYRIEN 54
|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 67 MQKFLGLEVTCKLSDTLEVMRKPCGVDPDVGHFTFPGIKPWRKTHTLVYIVN 120

RESULT 9
KCRESI
Stromelysin 1 (EC 3.4.24.17) precursor - rabbit
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A37306; A29157
R:Fini, M.E.; Karmaliowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckherhoff, C Arthritis Rheum. 30, 1254-1264, 1987

RESULT 12

KCRTIH

stromelysin 1 (EC 3.4.24.17) precursor - rat
N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A00997; PS0150; S22767
R;Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A;Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A;Reference number: A00997; MUID:85284930; PMID:3875482
A;Accession: A00997
A;Molecule type: mRNA
A;Residues: 1-475 <MAL>
A;Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIDN:CAA26448.1; PID:G57461
R;Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A;Title: Purification and properties of extracellular matrix-degrading metallo-proteinase
A;Reference number: PS0150; MUID:91154156; PMID:1963430
A;Accession: PS0150
A;Molecule type: protein
A;Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UME>
R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A;Reference number: A26403; MUID:87146421; PMID:3547333
A;Contents: annotation; introns
A;Note: Intron positions were determined by comparison of the previously reported cDNA s
R;Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
J. Biol. Chem. 263, 11892-11899, 1988
A;Title: Structure-function relationships in the collagenase family member transin.
A;Reference number: S22767; MUID:98298869; PMID:2841336
A;Contents: annotation; active site; activation
A;Note: molecules with mutations in the autoinhibitory region showed a much increased te
A;Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme
R;Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
J. Biol. Chem. 266, 1584-1590, 1991
A;Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon
A;Reference number: A43028; MUID:91107652; PMID:1988438
A;Contents: annotation; autoinhibitory region
A;Note: Arg-89 and Cys-92 are essential for maintaining latency
C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C;Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit
C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C;Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi
C;Genetics: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
C;Function:
A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-475/Product: prostromelysin 1 #status predicted <PRO>
F;18-97/Domain: activation peptide #status predicted <ACT>
F;58-262/Domain: matrix metalloproteinase homology <MMP>
F;88-95/Region: autoinhibitory
F;98-475/Product: stromelysin 1 #status predicted <MAT>
F;282-475/Domain: hemopexin repeat homology <PXN>
F;90,216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;118/Binding site: carboxylate (Asn) (covalent) #status predicted
F;216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
F;217/Active site: Glu #status experimental
F;288-475/Disulfide bonds: #status predicted

Query Match 58.9%; Score 172; DB 1; Length 475;
Best Local Similarity 53.7%; Pred. No. 2e-13;
Matches 29; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 65 MQKFLGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 118

RESULT 13

JC5743

matrix metalloproteinase (EC 3.4.24.-) precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 09-Dec-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C;Accession: JC5743
R;Bartlett, J.D.; Slimmer, J.P.; Xue, J.; Margolis, H.C.; Moreno, E.C.
Gene 183, 123-128, 1996
A;Title: Molecular cloning and mRNA tissue distribution of a novel matrix metalloprotein
A;Reference number: JC5743; MUID:97149286; PMID:8996096
A;Accession: JC5743
A;Molecule type: mRNA
A;Residues: 1-483 <BAR>
A;Cross-references: UNIPROT:P79287; GB:U54825; NID:G1800212; PIDN:AAB41396.1; PID:G18002
A;Experimental source: enamel organ
C;Comment: This enzyme plays a role in enamel biomineralization and development.
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: hydrolase; metalloproteinase; zinc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-483/Product: matrix metalloproteinase #status predicted <MAT>
F;68-271/Domain: matrix metalloproteinase homology <MMP>
F;290-483/Domain: hemopexin repeat homology <PXN>
F;100,226,230,236/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;226,230,236/Binding site: zinc, catalytic (His) #status predicted
F;227/Active site: Glu #status predicted

Query Match 58.9%; Score 172; DB 2; Length 483;
Best Local Similarity 59.8%; Pred. No. 2e-13;
Matches 31; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 52

Db 75 LQAFGLVTKGLDRTMDVIKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 126

RESULT 14

S29243

interstitial collagenase (EC 3.4.24.7) precursor - mouse
N;Alternate names: matrix metalloproteinase 1 (MMP1)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S29243
R;Henriët, P.; Rousseau, G.G.; Eckhout, Y.
FEBS Lett. 310, 175-178, 1992
A;Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat c
A;Reference number: S29243; MUID:93011910; PMID:1383028
A;Accession: S29243
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <HEN>
A;Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G53604
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;65-268/Domain: matrix metalloproteinase homology <MMP>
F;279-472/Domain: hemopexin repeat homology <PXN>
F;97,223,227,233/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted
F;224/Active site: Glu #status predicted

Query Match 57.5%; Score 168; DB 2; Length 472;
Best Local Similarity 57.4%; Pred. No. 6.2e-13;
Matches 31; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 72 MQSFGLEVTKGLDDPTLDMRKPCGVPDVGSEYVFPRTLKWSQTNLTIRYN 125

RESULT 15

KCRTS2

stromelysin 2 (EC 3.4.24.22) precursor - rat

Search completed: May 27, 2005, 07:13:34
Job time : 21.4231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 94.5 Seconds
(without alignments)

292.617 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	469	1 MM01 HUMAN	P03956 homo sapien
2	283	96.9	468	1 MM01 RABIT	P13943 oryctolagus
3	279	95.5	469	1 MM01 HORSE	O9XS25 equus caball
4	270	92.5	469	1 MM01 PIG	P21692 sus scrofa
5	234	80.1	469	1 MM01 BOVIN	P28053 bos taurus
6	231.5	79.3	384	1 MM01 RANCA	Q11133 rana catesb
7	214	73.3	467	1 MM08 HUMAN	P22894 homo sapien
8	204	69.9	205	2 Q810Z2	Q81022 mus musculus
9	204	69.9	463	2 Q9EPL6	Q9EPL6 mus musculus
10	204	69.9	464	2 Q9EPL5	Q9EPL5 mus musculus
11	196	67.1	466	1 MM08 RAT	O88766 rattus norv
12	189	64.7	476	1 MM10 HUMAN	P09238 homo sapien
13	189	64.7	477	1 MM03 HUMAN	P08254 homo sapien
14	189	64.7	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
15	186	63.7	145	2 Q9N283	Q9N283 bos taurus
16	186	63.7	393	2 Q8M118	Q8M118 felis silve
17	186	63.7	478	1 MM03 RABIT	P28863 oryctolagus
18	184	63.0	252	2 Q6PMQ3	Q6PMQ3 xenopus lae
19	184	63.0	259	2 Q7ZT19	Q7ZT19 xenopus lae
20	183	62.7	472	2 Q93342	Q93342 gallus gall
21	183	62.7	477	1 MM03 HORSE	O28397 equus cabal
22	181	62.0	466	2 Q7SVX1	Q7SVX1 xenopus lae
23	180	61.6	259	2 Q7SZT5	Q7SZT5 xenopus lae
24	179	61.3	458	2 Q6DCN8	Q6DCN8 xenopus lae
25	178	61.0	258	2 Q7SZS8	Q7SZS8 xenopus lae
26	178	61.0	259	2 Q6DF35	Q6DF35 xenopus tro
27	178	61.0	481	1 MM20 BOVIN	O18767 bos taurus
28	176	60.3	465	2 Q8C309	Q8C309 mus musculus
29	176	60.3	465	2 Q8C330	Q8C330 mus musculus
30	176	60.3	471	1 MM13 RABIT	O62806 oryctolagus
31	174	59.6	167	2 Q7ZWD0	Q7ZWD0 brachydanio

32 174 59.6 482 1 MM20 MOUSE P57748 mus musculus
33 173 59.2 476 1 MM10 MOUSE O55123 mus musculus
34 173 59.2 477 1 MM03 MOUSE P28862 mus musculus
35 173 59.2 479 2 Q922K6 Q922K6 mus musculus
36 172 58.9 475 1 MM03 RAT P03957 rattus norv
37 172 58.9 483 1 MM20 HUMAN O60882 homo sapien
38 172 58.9 483 1 MM20 PIG P79287 sus scrofa
39 172 58.9 483 2 Q6DKT9 Q6DKT9 homo sapien
40 171 58.6 471 2 Q98959 Q98959 cynops pyrr
41 170 58.2 139 2 Q9GM68 Q9GM68 sus scrofa
42 168 57.5 452 2 Q9TT82 Q9TT82 canis fami
43 168 57.5 465 1 MM08 MOUSE O70138 mus musculus
44 168 57.5 472 1 MM13 MOUSE P33435 mus musculus
45 167.5 57.4 475 2 Q9DBE0 Q9DBE0 oncothynchu

ALIGNMENTS

RESULT 1
MM01_HUMAN
ID MM01_HUMAN STANDARD; PRT; 469 AA.
AC P03956; P08156;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90352587; PubMed=2167156;
RA Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,
RA Stetler-Stevenson W.G.;
RT "Cloning and characterization of human tumor cell interstitial
RT collagenase";
RL Cancer Res. 50:5431-5437 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis";
RL Biochem. J. 240:913-916 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196089; PubMed=3009463;
RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,
RA Eisen A.Z.;
RT "Human fibroblast collagenase. Complete primary structure and homology
RT to an oncogene transformation-induced rat protein.";
RL J. Biol. Chem. 261:6600-6605 (1986).
RN [4]
RP SEQUENCE FROM N.A.
RX Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RN MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalilus D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.;
RA "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RA collagenase gene is mediated by an inducible enhancer element located
RA in the 5'-flanking region.";
RL Mol. Cell. Biol. 7:2256-2266(1987).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RC TTSUE-Synovial cell;
RX MEDLINE=87109799; PubMed=3027129;
RA Brinckethoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
RA "Molecular cloning of human synovial cell collagenase and selection of
RA a single gene from genomic DNA.";
RL J. Clin. Invest. 79:542-546(1987).
RN [8]
RP SEQUENCE OF 100-112 AND 270-287.
RC TTSUE=Fibroblast;
RX MEDLINE=87194799; PubMed=3032950;
RA Clark I.M., Cawston T.E.;
RA "Fragments of human fibroblast collagenase. Purification and
RA characterization.";
RL Biochem. J. 263:201-206(1989).
RN [9]
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.;
RA "Human fibroblast collagenase contains an amino acid sequence
RA homologous to the zinc-binding site of Serratia protease.";
RL J. Biol. Chem. 262:5943-5943(1987).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.;
RA "Structure of the catalytic domain of human fibroblast collagenase
RA complexed with an inhibitor.";
RL Nat. Struct. Biol. 1:106-110(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
RA "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RA complexed to itself.";
RL Biochemistry 33:8207-8217(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.;
RA "Structure of the catalytic domain of fibroblast collagenase complexed
RA with an inhibitor.";
RL Science 263:375-377(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
RA "1.56-A structure of mature truncated human fibroblast collagenase.";
RN Proteins 19:98-109(1994).
RL [14]
RP STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219; DOI=10.1021/bi972181w;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.;
RA "High-resolution solution structure of the inhibitor-free catalytic
RA fragment of human fibroblast collagenase determined by
RA multidimensional NMR.";
RL Biochemistry 37:1495-1504(1998).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC -!- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05231; CAA28858.1; -
DR EMBL; M13509; AAA35699.1; -
DR EMBL; M16567; AAA52033.1; -
DR EMBL; U78045; AAB36941.1; -
DR EMBL; BC013875; AAB13875.1; -
DR EMBL; M15996; AAA35700.1; -
DR EMBL; X54925; CAA38691.1; -
DR PIR; A37308; KCHUI.
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGE; X-ray; @=102-269.
DR PDB; 1CGF; X-ray; A/B=102-263.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -
DR GlycoSuiteDB; P03956; -
DR Genew; HGNC:7155; MMP1.
DR H-InvDB; HIX0010067; -
DR MIM; 120353; -
DR GO; GO:0008133; F:collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.

ID AC 09X5Z5; STANDARD; PRT; 469 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).
 DE metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Richardson D.W.;
 RT "Cloning and expression of equine matrix metalloproteinase 1 (interstitial collagenase).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X. collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the activation peptide.
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC
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 CC
 CC EMBL; AF148882; AAD38030.1; --
 DR HSP; P03956; IAYK.
 DR MEROPS; M10.001; --
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR009070; PGHD like.
 DR Pfam; PF00045; Hemopexin_4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HK; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT METAL 124 124 Calcium 1 (By similarity).
 FT METAL 158 158 Calcium 2 (By similarity).
 FT METAL 168 168 Zinc 1 (By similarity).
 FT METAL 170 170 Zinc 1 (By similarity).
 FT METAL 175 175 Calcium 3 (By similarity).
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).

FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 183 183 Zinc 1 (By similarity).
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 194 194 Calcium 2 (By similarity).
 FT METAL 196 196 Zinc 1 (By similarity).
 FT METAL 198 198 Calcium 3 (By similarity).
 FT METAL 199 199 Calcium 1 (By similarity).
 FT METAL 201 201 Calcium 3 (By similarity).
 FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
 FT ACT_SITE 219 219 By similarity.
 FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
 FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT DISULFID 278 466 By similarity.
 SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;
 Query Match 95.5%; Score 279; DB 1; Length 469;
 Best Local Similarity 94.4%; Pred. No. 1.8e-27;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MOEFGLKVTGPDATLKVMTQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 DB 67 MOEFGLKVTGPDATLKVMTQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
 RESULT 4
 MM01_PIG STANDARD; PRT; 469 AA.
 AC P21692;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=9133421; PubMed=1651440;
 RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
 RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of expression of RNA in vitro by various cytokines.";
 RL Matrix 11:161-167(1991).
 RN [2]
 RP SEQUENCE OF 25-469 FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=91067477; PubMed=2174547;
 RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
 RT "Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.";
 RL Nucleic Acids Res. 18:6703-6703(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
 RX MEDLINE=96173003; PubMed=8590015; DOI=10.1016/S0969-2126(01)00188-5;
 RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A., Clark I.M., Blegg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
 RT "Structure of full-length porcine synovial collagenase reveals a C-

terminal domain containing a calcium-linked, four-bladed beta-propeller.";
 RT Structure 3:541-549(1995).
 RL [4]
 RN SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
 RP MEDLINE=95142615; PubMed=7840605; DOI=10.1006/abbi.1995.1018;
 RX Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
 RA O'Hare M.C.;
 RT "Recombinant porcine collagenase: purification and autolysis.";
 RL Arch. Biochem. Biophys. 316:123-127(1995).
 CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-I-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where Pl' is a
 CC hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -1- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment
 CC having reduced collagenolytic activity.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X54724; CAA38526.1; -;
 DR PIR; S15986; KCPGI.
 DR PDB; 1FBL; X-ray; @=100-469.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR009070; PGSD like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
 KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19
 FT PROPEP 20 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT CHAIN 100 258 18 kDa interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT SITE 258 259 Cleavage (autolytic).
 FT METAL 124 124 Calcium 1.
 FT METAL 158 158 Calcium 2.
 FT METAL 168 168 Zinc 1.
 FT METAL 170 170 Zinc 1.
 FT METAL 175 175 Calcium 3.
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
 FT METAL 183 183 Zinc 1.
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
 FT METAL 194 194 Zinc 1.
 FT METAL 196 196 Calcium 3.
 FT METAL 198 198 Calcium 1.
 FT METAL 199 199 Calcium 3.
 FT METAL 201 201 Calcium 3.
 FT METAL 218 218 Zinc 2 (catalytic).
 FT ACT_SITE 219 219 Zinc 2 (catalytic).
 FT METAL 222 222 Zinc 2 (catalytic).
 FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
 FT DISULFID 478 466 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120
 FT STRAND 101 102
 FT TURN 104 105
 FT STRAND 113 118
 FT TURN 123 124
 FT HELIX 127 142
 FT TURN 143 144
 FT STRAND 148 152
 FT STRAND 159 164
 FT STRAND 182 184
 FT TURN 190 193
 FT STRAND 195 198
 FT TURN 199 200
 FT STRAND 204 204
 FT STRAND 211 211
 FT HELIX 212 223
 FT TURN 224 225
 FT STRAND 226 227
 FT TURN 232 233
 FT TURN 235 236
 FT HELIX 250 260
 FT TURN 277 278
 FT TURN 280 281
 FT STRAND 286 290
 FT TURN 291 292
 FT STRAND 293 298
 FT TURN 299 300
 FT STRAND 301 305
 FT STRAND 313 316
 FT HELIX 317 320
 FT STRAND 330 334
 FT TURN 335 338
 FT STRAND 339 344
 FT TURN 345 346
 FT STRAND 347 352
 FT TURN 353 354
 FT STRAND 355 356
 FT TURN 358 359
 FT STRAND 362 363
 FT HELIX 364 368
 FT TURN 372 373
 FT STRAND 379 383
 FT TURN 384 387
 FT STRAND 388 393
 FT TURN 394 395
 FT STRAND 396 401
 FT TURN 402 405
 FT STRAND 406 407
 FT STRAND 413 414
 FT HELIX 415 418
 FT TURN 420 421
 FT STRAND 428 432
 FT TURN 433 434
 FT STRAND 435 440
 FT TURN 441 442
 FT STRAND 443 448
 FT TURN 449 452
 FT STRAND 453 459

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FT TURN 460 461
FT HELIX 462 464
FT TURN 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 92.5%; Score 270; DB 1; Length 469;
Best Local Similarity 90.7%; Pred. No. 2.6e-26;
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 5
MM01_BOVIN STANDARD; PRT; 469 AA.
ID MM01_BOVIN
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periodontium fibroblast;
RX MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence.";
RL DNA Seq. 5:63-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=131165;
RA Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D.,
RA Parke W.C.;
RT "Purification and characterization of bovine interstitial collagenase
RT and tissue inhibitor of metalloproteinases.";
RL Arch. Biochem. Biophys. 293:370-376(1992).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagenially one bond in native
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58256; CAA41210.1; -.
CC F01; S14654; KCB01.
CC HSSP; P03956; 1HFC.
CC MEROPS; M10.001; -.
CC InterPro; IPR000585; Hemopexin.

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DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRILIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZMGC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Direct protein sequencing;
KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 18
FT PROPEP 19 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 199 199 Calcium 1 (By similarity).
FT METAL 201 201 Calcium 3 (By similarity).
FT METAL 218 218 Zinc 2 (Catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (Catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (Catalytic) (By similarity).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT DISULFID 278 466 By similarity.
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CONFLICT 22 23 AT -> FP (in Ref. 2).
FT CONFLICT 30 30 D -> L (in Ref. 2).
FT CONFLICT 35 36 KK -> LL (in Ref. 2).
FT CONFLICT 85 85 N -> F (in Ref. 2).
FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
FT CONFLICT 113 113 N -> D (in Ref. 2).
SQ SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;

Query Match 80.1%; Score 234; DB 1; Length 469;
Best Local Similarity 81.5%; Pred. No. 1.2e-21;
Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

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RESULT 6
MM01_RANCA STANDARD; PRT; 384 AA.
ID MM01_RANCA
AC Q11133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (TCL).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=9400;
RN [1]
SEQUENCE FROM N.A.
RC MEDLINE=95071832; PubMed=7981043;
RC TISSUE=Skin;
RA Oafusa K. Yomori S., Yoshizato K.;
RT "Regionally and hormonally regulated expression of genes of collagen
RT and collagenase in the anuran larval skin.";
RL Int. J. Dev. Biol. 38:345-350(1994).
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-[Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC EMBL; S75623; AAB32661.1; --
CC PIR; I51267; I51267.
CC HSP; P21692; IPBL.
CC MEROPS; M10.001; --
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR01818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR006026; PeptIdase_M.
CC InterPro; IPR009070; PGSD_like.
CC Pfam; PF00045; Hemopexin; 2.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00138; MATRIXIN.
CC SMART; SM00120; HX; 2.
CC SMART; SM00235; ZMNC; 1.
CC PROSITE; PS00546; CYSTEINE SWITCH; FALSE_NEG.
CC PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Extracellular matrix;
CC Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 25 Potential.
FT PROPEP 26 88 Activation peptide (Potential).
FT FT CHAIN 89 384 Interstitial collagenase.
FT DOMAIN 239 384 Hemopexin-like.
FT SITE 81 81 Cysteine switch (Potential).
FT METAL 113 113 Calcium 1 (By similarity).
FT METAL 129 129 Calcium 2 (By similarity).
FT METAL 139 139 Zinc 1 (By similarity).
FT METAL 141 141 Zinc 1 (By similarity).

```

RC TISSUE=Neutrophils;
RX MEDLINE=92111500; PubMed=1662606;
RA Blaeser J., Knaeuper V., Oeschues A., Reinke H., Tschesche H.;
RT "Mercurial activation of human polymorphonuclear leucocyte
RT procollagenase.";
RL Eur. J. Biochem. 202;1223-1230(1991).
RN [4]
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
RC TISSUE=Neutrophils;
RX MEDLINE=91104978; PubMed=2176876;
RA Maliya S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,
RA Birkedal-Hansen H., van Wart H.E.;
RT "Characterization of 58-kilodalton human neutrophil collagenase:
RT comparison with human fibroblast collagenase.";
RL Biochemistry 29:10628-10634(1990).
RN [5]
RN PARTIAL SEQUENCE.
RX MEDLINE=90380298; PubMed=2169256;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).
RN [7]
RN CYSTEINE-SWITCH MECHANISM.
RC TISSUE=Neutrophils;
RX MEDLINE=93050220; PubMed=1330697; DOI=10.1016/0014-5793(92)81184-N;
RA Blaeser J., Triebel S., Reinke H., Tschesche H.;
RT "Formation of a covalent Hg-Cys-bond during mercurial activation of
RT PMNL procollagenase gives evidence of a cysteine-switch mechanism.";
RL FEBS Lett. 313:59-61(1992).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
RX MEDLINE=94185631; PubMed=8137810;
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
RT "The X-ray crystal structure of the catalytic domain of human
RT neutrophil collagenase inhibited by a substrate analogue reveals the
RT essentials for catalysis and specificity.";
RL EMBO J. 13:1263-1269(1994).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
RX MEDLINE=94139300; PubMed=8307185; DOI=10.1016/0014-5793(94)80370-6;
RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
RA Tschesche H., Bode W.;
RT "Structural implications for the role of the N terminus in the
RT 'superactivation' of collagenases. A crystallographic study.";
RL FEBS Lett. 338:227-233(1994).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
RX MEDLINE=95384762; PubMed=7656015;
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
RA Oronfleh M.W., Banks T.M., Rubin B.;
RT "Structure of human neutrophil collagenase reveals large S1'
RT specificity pocket.";
RL Nat. Struct. Biol. 1:119-123(1994).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
RX MEDLINE=97390108; PubMed=9249047;
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
RA Bode W., Gomis-Ruth F.-X.;
RT "1.8-A crystal structure of the catalytic domain of human neutrophil
RT collagenase (matrix metalloproteinase-8) complexed with a
RT peptidomimetic hydroxamate primed-side inhibitor with a distinct
RT selectivity profile.";
RL Eur. J. Biochem. 247:356-363(1997).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
RX MEDLINE=98318039; PubMed=9655333;
RA Brandstetter H., Engh R.A., von Roeder E.G., Moroder L., Huber R.,
RA Bode W., Grams F.;

RT "Structure of malonic acid-based inhibitors bound to human neutrophil
RT collagenase. A new binding mode explains apparently anomalous data.";
RL Protein Sci. 7:1303-1309(1998).
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
CC type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
CC -!- ENZYME REGULATION: Cannot be activated without removal of the
CC activation peptide.
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- TISSUE SPECIFICITY: Neutrophils.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J05556; AAA88021.1; -.
DR PIR; A37073; KCHUN.
DR PDB; 1A85; X-ray; A=105-262.
DR PDB; 1A86; X-ray; A=105-262.
DR PDB; 1B25; X-ray; A=99-263.
DR PDB; 1I73; X-ray; A=100-262.
DR PDB; 1I76; X-ray; A=100-262.
DR PDB; 1JAN; X-ray; A=99-262.
DR PDB; 1JAO; X-ray; A=100-262.
DR PDB; 1JAP; X-ray; A=100-262.
DR PDB; 1JAH; X-ray; A=105-262.
DR PDB; 1JH1; X-ray; A=105-262.
DR PDB; 1JH9; X-ray; A=100-262.
DR PDB; 1KBC; X-ray; A/B=99-262.
DR PDB; 1MNB; X-ray; @=100-262.
DR PDB; 1MNC; X-ray; @=101-263.
DR MEROPS; M10.002; -.
DR Genew; HGNC:7175; MMP8.
DR MIM; 120355; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008130; F:neutrophil collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0008508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
KW SIGNAL 1 20
FT PROPEP 21 100 Activation peptide.
FT CHAIN 101 467 Neutrophil collagenase.
FT DOMAIN 276 467 Hemopexin-like.
FT SITE 91 91 Cysteine switch.
FT METAL 157 157 Calcium 1.
FT METAL 167 167 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Zinc 1.


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FT METAL          189      189   Calcium 1 (via carbonyl oxygen).
FT METAL          191      191   Calcium 1 (via carbonyl oxygen).
FT METAL          193      193   Calcium 1.
FT METAL          195      195   Zinc 1.
FT METAL          197      197   Calcium 2.
FT METAL          200      200   Calcium 2.
FT METAL          217      217   Zinc 2 (catalytic).
FT ACT_SITE       218      218
FT METAL          221      221   Zinc 2 (catalytic).
FT METAL          227      227   Zinc 2 (catalytic).
FT METAL          286      286   Calcium 3 (via carbonyl oxygen) (By similarity).
FT FT            378      378   Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL          425      425   Calcium 3 (via carbonyl oxygen) (By similarity).
FT FT CARBOHYD     54        54    N-linked (GlcNAc . . ) (Probable).
FT FT CARBOHYD     73        73    N-linked (GlcNAc . . ) (Probable).
FT FT CARBOHYD    112       112    N-linked (GlcNAc . . ).
FT FT CARBOHYD    204       204    N-linked (GlcNAc . . ) (Potential).
FT FT CARBOHYD    246       246    N-linked (GlcNAc . . ) (Potential).
FT FT DISULFID    279       279    Probable.

Query Match              73.3%; Score 214; DB 1; Length 467;
Best Local Similarity    70.4%; Pred.No. 4.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQBFFGLKVTGPKDAETLKYMKPRCGVPDDVAQFLTEGNRWEQHLYTYRIEN 54
DB 66 MQRFPLNLVTKPNEELDMWKRCPCGVPSGGFMLTPGFKPWERTNLTYYRIIN 119

RESULT 8
QB10Z2 PRELIMINARY; PRT; 205 AA.
AC QB10Z2 AC QB10Z2 PRELIMINARY; PRT; 205 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SwJ;
RA Brathwaite M., Waeltz P., Nagaraja R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY211543; AAC37594.1; -.
DR HSPG; PO8254; ISLM.
DR MEROPS; M10_034; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR DR InterPro; IPRO06026; Peptidase M.
DR InterPro; IPRO01818; Pept_M10A_M12B.
DR InterPro; IPRO09070; PGBD_like
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SMO0235; ZnMG; 1.
DR PROSITE; PS00546; CVSTEINE_SWITCH; 1.
KW Collagen.
KN NON_TER
SQ SEQUENCE 205 AA; 23403 MW; DEDLE974E8769643 CRC64;
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DR MEROPS; M10.002; --
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PF00138; MATRINXIN.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By similarity).
FT DISULFID 280 465 Probable.
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE9756E76C90 CRC64;

Query Match 67.1%; Score 196; DB 1; Length 466;
Best Local Similarity 63.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKPCGVPDVAOVFLTEGPNRWEQTHLYRIEN 54
DB 67 MQRFVGLPETGKPDATIEIMKPCGVPDSDGDFLLTPGSPKWTNLTLYRIIN 120

RESULT 12
MM10_HUMAN
ID MM10_HUMAN STANDARD; PRT; 476 AA.
AC P09238;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
GN (MMP-10) (Transin-2) (SL-2).
Name=MMP10; Synonyms=STMY2;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88339885; PubMed=2844164;
RA Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.,
RA Breathnach R.;
RT "The collagenase gene family in humans consists of at least four
RT members.";
RL Biochem. J. 253:187-192(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,
CC and V; weakly collagens III, IV, and V. Activates procollagenase.
CC -1- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on
CC collagen types III, IV and V is weak.
CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
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CC -----
DR EMBL; X07820; CAA30679.1; --
DR EMBL; BC002591; AAH02591.1; --
DR PIR; A28816; KCHUS2.
DR HSP; P08254; IG05.
DR MEROPS; M10.006; --
DR Genew; HGNC:7156; MMP10.
DR H-InvDB; HIX0010066; --
DR MIM; 185260; --
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR006036; Peptidase_M.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.

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DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPP 18 98 Activation peptide.
FT CHAIN 99 476 Stromelysin-2.
FT DOMAIN 286 476 Hemopexin-like.
FT SITE 91 91 Cysteine switch (By similarity).
FT METAL 217 217 Zinc (catalytic) (By similarity).
FT ACT_SITE 218 218 By similarity.
FT METAL 221 221 Zinc (catalytic) (By similarity).
FT METAL 227 227 Zinc (catalytic) (By similarity).
FT DISULFID 289 476 By similarity.
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDPEF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 1; Length 476;
Best Local Similarity 63.0%; Pred. No. 8.8e-16;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVKTPGDAETLKMVKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 MQKFLGLEVTGKLDITLTVEMRKPCGVPDVGHFSPGMPKWKTHLYRIVN 119

RESULT 13
MM03 HUMAN STANDARD; PRT; 477 AA.
AC P08254;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1).
GN Name=MMP3; Synonyms=STMV1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
RX MEDLINE=88198243; PubMed=3360803;
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
RA Kurkinen M.;
RT "The complete primary structure of human matrix metalloproteinase-3.
RT Identity with stromelysin.";
RL J. Biol. Chem. 263:6742-6745 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis.";
RL Biochem. J. 240:913-916 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016164; PubMed=3477804;
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,
RA Grant G.A., Bauer E.A., Goldberg G.I.;
RT "Human skin fibroblast stromelysin: structure, glycosylation,
RT substrate specificity, and differential expression in normal and
RT tumorigenic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,

RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-
RT PHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RN ZYMOGEN ACTIVATION.
RX MEDLINE=90344802; PubMed=2383557;
RA Nagase H., Engchild J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix
RT metalloproteinase 3 (stromelysin) by proteinases and (4-
RT aminophenyl)mercuric acetate.";
RL Biochemistry 29:5783-5789 (1990).
RN [7]
RN STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RX MEDLINE=95384761; PubMed=7656014;
RA Cooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
RA Johnson B.A.;
RT "The NMR structure of the inhibited catalytic domain of human
RT stromelysin-1.";
RL Nat. Struct. Biol. 1:111-118 (1994).
RN [8]
RN STRUCTURE BY NMR OF 100-267.
RX MEDLINE=99043696; PubMed=9827994;
RA Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A.,
RA Kloosterman D.A., Mizzak S.A., Jacobsen E.J., Belonga K.L.,
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
RA Ledbetter S.R., Kaytes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
RA Poorman R.A.;
RT "Solution structures of stromelysin complexed to thiadiazole
RT inhibitors.";
RL Protein Sci. 7:2281-2286 (1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
RX MEDLINE=96117647; PubMed=8535233;
RA Becker J.W., Marcy A.I., Rokos L.L., Axel M.G., Burbaum J.J.,
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
RA Hermes J.D., Springer J.P.;
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
RT domain and of the C-truncated proenzyme.";
RL Protein Sci. 4:1966-1976 (1995).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.
RX MEDLINE=96311273; PubMed=8740360; DOI=10.1016/S0969-2126(96)00043-3;
RA Dhanraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.F.,
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin
RT catalytic domain and its comparison with members of the zinc
RT metalloproteinase superfamily.";
RL Structure 4:375-386 (1996).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
RX MEDLINE=97236965; PubMed=9083493; DOI=10.1021/jm960465t;
RA Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L.,
RA Girotra N.N., Kopka I.E., Lanza T.J., LeVorse D.A., Maccoss M.,
RA Owens K.A., Ponipom M.M., Simeone J.P., Harrison R.K.,
RA Niedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,
RA McDonnell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M.,
RA Shen F., Colletti A., Krieter P.A., Hagmann W.K.;
RT "Inhibition of stromelysin-1 (MMP-3) by pI'-biphenylylethyl
RT carboxyalkyl dipeptides.";
RL J. Med. Chem. 40:1026-1040 (1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH
RP TIMP1.
RX MEDLINE=97433330; PubMed=9288970; DOI=10.1038/37995;
RA Gomis-Rueth F.-X., Maskos K., Betz M., Bergner A., Huber R.,

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DR PDB; 1DSF; X-ray; A/B=100-272.
DR PDB; 1D8M; X-ray; A/B=100-272.
DR PDB; 1G05; X-ray; A/B=100-272.
DR PDB; 1G45; X-ray; A/B=100-272.
DR PDB; 1G4K; X-ray; A/B=100-272.
DR PDB; 1G4X; X-ray; A/B/C=100-267.
DR PDB; 1HFS; X-ray; @=105-264.
DR PDB; 1HY7; X-ray; A/B=100-272.
DR PDB; 1HW7; X-ray; A/B=100-272.
DR PDB; 1MW7; Model; A=100-268.
DR PDB; 1OO9; NMR; A=100-267.
DR PDB; 1QAA; X-ray; A/B/C/D=106-267.
DR PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR PDB; 1SLM; X-ray; @=18-272.

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Best Local Similarity 63.0%; Pred.No.8.e-16;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY      1 MQEFGGLKVTGKDASTLKVMPKPGCVDPVAQFVLTEGNPRVEQTHLTYYRIEN 54
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Db       67 MQKFLELVGTGVSDTLVWRKPRCGVPDVGHFRTPFGIPKWKRTHTLYRIVN 120

RESULT 14
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ID Q6Y4Q5 AC Q6Y4Q5 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Names=WMEF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AV183143; AAC63580.1; -.
DR HSSP; P08254; IBD3.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR01818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR009070; PGBD like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
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Db       67 MQKFLELVGTGVSDTLAMRRPRCGVPDVGDFTTFFGMPKWKRTHTLYRIVN 120

RESULT 15
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ID Q9N283 AC Q9N283 DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Names=WMEF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AV183143; AAC63580.1; -.
DR HSSP; P08254; IBD3.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR01818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR009070; PGBD like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;

Query Match          64.7%; Score 189; DB 2; Length 478;
Best Local Similarity 61.1%; Pred.No.8.e-16;
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QY      1 MQEFGGLKVTGKDASTLKVMPKPGCVDPVAQFVLTEGNPRVEQTHLTYYRIEN 54
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Db       67 MQKFLELVGTGVSDTLAMRRPRCGVPDVGDFTTFFGMPKWKRTHTLYRIVN 120

RESULT 15
Q9N283 PRELIMINARY; PRT; 145 AA.
ID Q9N283 AC Q9N283 DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Names=WMEF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AV183143; AAC63580.1; -.
DR HSSP; P08254; IBD3.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR01818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR009070; PGBD like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;
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 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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 GN Name=bmp-3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
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 RA Sato T., Hirata M., Ito A., Hashizume K.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
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 DR MEROPS; M10.006; -.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
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Search completed: May 27, 2005, 06:57:32
 Job time : 95.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 104.885 seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFLKVTGRPAETLVK.....VLTEGPNRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17092 Human mat
4	292	100.0	454	7	ADE16002 G-coupled
5	292	100.0	454	7	ADE16004 G-coupled
6	292	100.0	454	7	ADE16008 G-coupled
7	292	100.0	454	7	ADE16006 G-coupled
8	292	100.0	454	8	ADL93945 Human G-c
9	292	100.0	454	8	ADL93943 Human G-c
10	292	100.0	455	8	ADL93941 Human G-c
11	292	100.0	469	4	AAB84606 Amino aci
12	292	100.0	469	4	AAE10415 Human mat
13	292	100.0	469	6	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU58596 Lung canc
18	292	100.0	469	6	ABU56597 Lung canc
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ADB79176 Matrix me
22	292	100.0	469	7	ADE34550 Human ski
23	292	100.0	469	7	ADE16000 G-coupled
24	292	100.0	469	7	ADE16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

ALIGNMENTS

RESULT 1

ABP97131
ID ABP97131 standard; peptide; 54 AA.

XX AC ABP97131;

XX XX AC (first entry)

DT 24-JUN-2003

DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.

XX Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.
XX Homo sapiens.

XX WO2003018748-A2.

XX 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

PR 21-DEC-2001; 2001US-00032376.

PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Weart IF;

XX WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological activities. (I) can be

Adn38694 Cancer/an
Adn38696 Cancer/an
Adn38698 Cancer/an
Adn38699 Human BEC
Adn38700 Human G-c
Adn38701 Human col
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Adn38974 Human col
Adn38975 Human col
Adn38976 Human col
Adn38977 Human col
Adn38978 Human col
Adn38979 Human col
Adn38980 Human col
Adn38981 Human col
Adn38982 Human col
Adn38983 Human col
Adn38984 Human col
Adn38985 Human col
Adn38986 Human col
Adn38987 Human col
Adn38988 Human col
Adn38989 Human col
Adn38990 Human col
Adn38991 Human col
Adn38992 Human col
Adn38993 Human col
Adn38994 Human col
Adn38995 Human col
Adn38996 Human col
Adn38997 Human col
Adn38998 Human col
Adn38999 Human col
Adn39000 Human col

DE G-coupled protein receptor related polypeptide, SEQ ID No 32.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
OS
OS Homo sapiens.
XX
PN WO200283841-A2.
XX
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 19-APR-2001; 2001US-0285609P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voas EZ, Vernet CAM, MacDougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Fatturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
XX WPI; 2003-067574/06.
XX N-PSDB; ADE16001.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 32; 32opp; English.
PS
XX The invention relates to a novel isolated G-coupled protein receptor
XX related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
XX Sequence 454 AA;
XX

Query Match 100.0%; Score 292; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. NO. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGPRWQTHLYRIEN 54
DB 50 MQEFFGLKVTGKPDATLKVWKQPCGVPDVAQFVLTEGPRWQTHLYRIEN 103

RESULT 5
ADE16004
ID ADE16004 standard; protein; 454 AA.
XX
AC ADE16004;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID No 34.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
XX WO200283841-A2.
XX
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 10-APR-2001; 2001US-0281906P.
PR 13-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX

PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 DR WPI; 2003-067574/06.
 DR N-PSDB; ADE16003.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 34; 320pp; English.
 XX
 PS The invention relates to a novel isolated G-coupled protein receptor
 XX related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification,
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeimic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 XX polypeptides of the invention.
 XX
 SQ Sequence 454 AA;
 Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103
 |||||
 RESULT 6
 ID ADE16008
 ID ADE16008 standard; protein; 454 AA.
 XX
 AC ADE16008;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE G-coupled protein receptor related polypeptide, SEQ ID No 38.
 XX
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeimic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

KW preventive medicine; pharmacogenomics; human.
 XX
 XX Homo sapiens.
 OS
 PN WO200283841-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010713.
 XX
 XX 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16007.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 XX Claim 1; SEQ ID NO 38; 320pp; English.
 PS
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification,
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeimic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 XX polypeptides of the invention.
 XX

CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

XX SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
 |||||
 Db 50 MQEFGGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

RESULT 7

ADAE16006

ID ADAE16006 standard; protein; 454 AA.

XX AC ADAE16006;

XX DT 29-JAN-2004 (first entry)

XX DE G-coupled protein receptor related polypeptide, SEQ ID No 36.

XX KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;

KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;

KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;

KW cell differentiation; cell proliferation; hematopoiesis; wound healing;

KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

KW preventive medicine; pharmacogenomics; human.

XX OS Homo sapiens.

XX PN WO200283841-A2.

XX PD 24-OCT-2002.

XX PF 03-APR-2002; 2002WO-US010713.

XX PR 03-APR-2001; 2001US-0281136P.

XX PR 05-APR-2001; 2001US-0281863P.

XX PR 05-APR-2001; 2001US-0281906P.

XX PR 10-APR-2001; 2001US-0282934P.

XX PR 13-APR-2001; 2001US-0283657P.

XX PR 13-APR-2001; 2001US-0283678P.

XX PR 13-APR-2001; 2001US-0283687P.

XX PR 13-APR-2001; 2001US-0283710P.

XX PR 17-APR-2001; 2001US-0284234P.

XX PR 19-APR-2001; 2001US-0285325P.

XX PR 20-APR-2001; 2001US-0285609P.

XX PR 23-APR-2001; 2001US-0285748P.

XX PR 23-APR-2001; 2001US-0285890P.

XX PR 24-APR-2001; 2001US-0286068P.

XX PR 27-APR-2001; 2001US-0287213P.

XX PR 03-MAY-2001; 2001US-0288509P.

XX PR 30-MAY-2001; 2001US-0294495P.

XX PR 31-MAY-2001; 2001US-0294801P.

XX PR 31-JUL-2001; 2001US-0309216P.

XX PR 25-SEP-2001; 2001US-0324775P.

XX PR 28-NOV-2001; 2001US-0333900P.

XX PR 02-APR-2002; 2002US-00115479.

XX PA (CURA-) CURAGEN CORP.

XX PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

PI Voss EZ, Vernet CAM, Macdonnell JR, Rastelli L, Anderson DW;

PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;

XX

DR WPI; 2003-067574/06.

XX N-PSDB; ADE16005.

XX PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemia, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.

XX PS Claim 1; SEQ ID NO 36; 320pp; English.

XX CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

XX SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
 |||||
 Db 50 MQEFGGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

RESULT 8

ADL93945

ID ADL93945 standard; protein; 454 AA.

XX AC ADL93945;

XX DT 20-MAY-2004 (first entry)

XX DE Human G-coupled protein receptor-related protein #18.

XX KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; scleroderma; obesity; transplacental;
 KW valve disease; tuberosus sclerosis; congenital adrenal hyperplasia; prostate cancer;
 KW adrenoleukodystrophy; lymphoma; uterus cancer; fertility;
 KW neoplasm; adenocarcinoma; idiopathic thrombocytopenic purpura;
 KW haemophilia; hypercoagulation; immunodeficiency; AIDS; bronchial asthma;
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
 KW neurodegenerative disorder; receptor.

OS Homo sapiens.
XX US2004006205-A1.
XX 08-JAN-2004.
XX 02-APR-2002; 2002US-00115479.
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 10-APR-2001; 2001US-0281906P.
XX 10-APR-2001; 2001US-0282934P.
XX 13-APR-2001; 2001US-0283577P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283687P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 23-APR-2001; 2001US-0285909P.
XX 23-APR-2001; 2001US-0286068P.
XX 24-APR-2001; 2001US-0287213P.
XX 27-APR-2001; 2001US-0287213P.
XX 03-MAY-2001; 2001US-0288509P.
XX 30-MAY-2001; 2001US-0294495P.
XX 31-MAY-2001; 2001US-0294801P.
XX 31-JUL-2001; 2001US-0309216P.
XX 25-SEP-2001; 2001US-0324775P.
XX 28-NOV-2001; 2001US-0333900P.
XX (LILL/) LI L.
XX (GERL/) GERLACH V.
XX (LIUX/) LIU X.
XX (MILL/) MILLER C E.
XX (SPYT/) SPYTEK K A.
XX (ZERH/) ZERHUSEN B D.
XX (PEN/) PENNA C E A.
XX (SHEN/) SHENOY S G.
XX (ZHON/) ZHONG H.
XX (SMIT/) SMITHSON G.
XX (CASH/) CASHMAN S J.
XX (BOLD/) BOLDOG F L.
XX (VOSS/) VOSS E Z.
XX (VERN/) VERNET C A.
XX (MACD/) MACDOUGALL J R.
XX (RAST/) RASTELLI L.
XX (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (MEZE/) MEZES P S.
XX (FURT/) FURTA K.
XX (PATT/) PATTURAJAN M.
XX (BURG/) BURGESS C E.
XX (MALY/) MALYANKAR U M.
XX (SHIM/) SHIMKETS R A.
XX (TAUP/) TAUPIER R J.
XX (EDIN/) EDINGER S.
XX (MAZU/) MAZUR A.
XX Li L, Gerlach V, Liu X, Miller CE, Spyttek KA, Zerkhusen BD;
XX Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
XX Voss EZ, Vernet C, MacDougall JR, Rastelli L, Anderson DW, Zhong M;
XX Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
XX Shimkets RA, Taupier RJ, Edinger S, Mazur A;
XX WPI; 2004-224146/21.
XX N-PSDB; ADL93944.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spyttek KA, Zerkhusen BD;
XX Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
XX Voss EZ, Vernet C, MacDougall JR, Rastelli L, Anderson DW, Zhong M;
XX Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
XX Shimkets RA, Taupier RJ, Edinger S, Mazur A;
XX WPI; 2004-224146/21.
XX N-PSDB; ADL93944.
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
XX treating or ameliorating, e.g. acquired immunodeficiency syndrome,
XX bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
XX scleroderma or obesity.
XX
XX Claim 1: Page 68: 220pp: English.

PR	27-APR-2001; 2001US-0287213P.	Matches	54;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
PR	03-MAY-2001; 2001US-0288509P.	Qy	1	MQEFFGLKVTGKPDATLKMVKQPRCGVPDVAQFVLTEGPNRWEQTHLTVRIEN	54						
PR	30-MAY-2001; 2001US-0294495P.	Db	50	MQEFFGLKVTGKPDATLKMVKQPRCGVPDVAQFVLTEGPNRWEQTHLTVRIEN	103						
PR	31-MAY-2001; 2001US-0294801P.										
PR	31-JUL-2001; 2001US-0309216P.										
PR	25-SEP-2001; 2001US-0324775P.										
PR	28-NOV-2001; 2001US-0333900P.										
XX		RESULT 10									
PA	(LILL/) LI L.	ADL93941									
PA	(GERL/) GERLACH V.	ID	ADL93941	standard; protein; 455 AA.							
PA	(LIUX/) LIU X.	XX									
PA	(MILL/) MILLER C E.	AC	ADL93941;								
PA	(SPYT/) SPYTEK K A.	XX									
PA	(ZERH/) ZERHUSEN B D.	DT	20-MAY-2004	(first entry)							
PA	(PENA/) PENA C E A.	XX									
PA	(SHEN/) SHENOY S G.	DE	Human G-coupled protein receptor-related protein #16.								
PA	(ZHON/) ZHONG H.	XX									
PA	(SMIT/) SMITHSON G.	XX									
PA	(CASM/) CASMAN S J.	KW	human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;								
PA	(BOLD/) BOLDOG F L.	KW	atherosclerosis; hypertension; congenital heart defect; aortic stenosis;								
PA	(VOSS/) VOSS E Z.	KW	atrial septal defect; atrioventricular canal defect; ductus arteriosus;								
PA	(VERN/) VERNET C A.	KW	pulmonary stenosis; subaortic stenosis; ventricular septal defect;								
PA	(MACD/) MACDOUGALL J R.	KW	valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;								
PA	(RAST/) RASTELLI L.	KW	adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;								
PA	(ANDE/) ANDERSON D W.	KW	neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;								
PA	(ZHON/) ZHONG M.	KW	haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;								
PA	(MEZE/) MEZES P S.	KW	immunodeficiency; graft versus host disease; AIDS; bronchial asthma;								
PA	(FURT/) FURTAK K.	KW	Crohn's disease; G-coupled protein receptor; metabolic disorder;								
PA	(PATY/) PATTURAJAN M.	XX	neurodegenerative disorder; receptor.								
PA	(BURG/) BURGESS C E.	OS	Homo sapiens.								
PA	(MALY/) MALYANKAR U M.	XX									
PA	(SHIM/) SHIMKETS R A.	PN	US2004006205-A1.								
PA	(TAUP/) TAUPIER R J.	XX									
PA	(EDIN/) EDINGER S.	XX									
PA	(MAZU/) MAZUR A.	PD	08-JAN-2004.								
XX		XX									
PI	Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;	PF	02-APR-2002; 2002US-00115479.								
PI	Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;	XX									
PI	Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;	PR	03-APR-2001; 2001US-0281136P.								
PI	Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;	PR	05-APR-2001; 2001US-0281863P.								
PI	Shimkets RA, Taupier RJ, Edinger S, Mazur A;	PR	05-APR-2001; 2001US-0281906P.								
XX	WPI; 2004-224146/21.	PR	10-APR-2001; 2001US-0282934P.								
DR	NF-PSDB; ADL93942.	PR	13-APR-2001; 2001US-0283657P.								
XX		PR	13-APR-2001; 2001US-0283678P.								
XX		PR	13-APR-2001; 2001US-0283710P.								
XX		PR	17-APR-2001; 2001US-0284234P.								
PT	New G-coupled protein-receptor related polypeptides, for preventing	PR	19-APR-2001; 2001US-0285325P.								
PT	treating or ameliorating, e.g. acquired immunodeficiency syndrome,	PR	20-APR-2001; 2001US-0285609P.								
PT	bronchial asthma, Crohn's disease, prostate cancer, hemophilia,	PR	23-APR-2001; 2001US-0285748P.								
PT	scleroderma or obesity.	PR	23-APR-2001; 2001US-0285890P.								
XX	Claim 1; Page 67; 220pp; English.	PR	24-APR-2001; 2001US-0286068P.								
PS		PR	27-APR-2001; 2001US-0287213P.								
XX		PR	03-MAY-2001; 2001US-0288509P.								
CC	The invention relates to isolated human G-coupled protein receptor-	PR	30-MAY-2001; 2001US-0294495P.								
CC	related polypeptides and polynucleotides. The proteins are useful for	PR	31-MAY-2001; 2001US-0294801P.								
CC	preventing, treating or ameliorating medical disorders by protein or gene	PR	31-JUL-2001; 2001US-0309216P.								
CC	therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,	PR	25-SEP-2001; 2001US-0324775P.								
CC	congenital heart defects, aortic stenosis, atrial septal defect,	XX									
CC	atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,										
CC	subaortic stenosis, ventricular septal defect, valve diseases, tubercu-										
CC	losclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,										
CC	congenital adrenal hyperplasia, prostate cancer, neoplasm,										
CC	adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,										
CC	hypercoagulation, idiopathic thrombocytopenic purpura,										
CC	immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,										
CC	metabolic disorders, neurodegenerative disorders or Crohn's disease. They										
CC	are also useful as diagnostic or research tools. The present sequence										
CC	represents a human G-coupled protein receptor-related protein of the										
CC	invention.										
XX											
SQ	Sequence 454 AA;										

Query Match 100.0%; Score 292; DB 8; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;


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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72663.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 735; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
RESULT 15
ABR58542
ID ABR58542 standard; protein; 469 AA.
XX
AC ABR58542;
XX
XX 09-JUL-2003 (first entry)
DT
DE Human cancer related protein SEQ ID NO:199.
DE
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
XX WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-US029560.
XX
XX 17-SEP-2001; 2001US-0323469P.

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PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72662.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 735; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
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Job time : 106.885 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:53:10 ; Search time 314.308 Seconds
(without alignments)
59.268 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 segs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	292	100.0	54	14	US-10-219-329-9
2	292	100.0	54	14	US-10-153-185-9
3	292	100.0	54	14	US-10-219-561-9
4	292	100.0	54	16	US-10-032-376A-9
5	292	100.0	54	16	US-10-335-207-9
6	292	100.0	454	15	US-10-115-479-32
7	292	100.0	454	15	US-10-115-479-34
8	292	100.0	454	15	US-10-115-479-36
9	292	100.0	454	15	US-10-115-479-38
10	292	100.0	469	9	US-09-391-104-23
11	292	100.0	469	9	US-09-801-196-19
12	292	100.0	469	9	US-09-853-386-100
13	292	100.0	469	14	US-10-301-822-119

14	292	100.0	469	14	US-10-021-660-76	Sequence 76, Appl
15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	15	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	15	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	15	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	15	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appl
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	469	17	US-10-901-417-23	Sequence 23, Appl
27	292	100.0	470	15	US-10-447-315-1	Sequence 1, Appl
28	292	100.0	496	14	US-10-106-698-6283	Sequence 6283, Ap
29	233	79.8	43	14	US-10-219-329-17	Sequence 17, Appl
30	233	79.8	43	14	US-10-153-185-17	Sequence 17, Appl
31	233	79.8	43	14	US-10-219-561-17	Sequence 17, Appl
32	233	79.8	43	16	US-10-032-376A-17	Sequence 17, Appl
33	233	79.8	43	16	US-10-335-207-17	Sequence 17, Appl
34	214	73.3	55	14	US-10-219-329-10	Sequence 10, Appl
35	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
36	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
37	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
38	214	73.3	55	16	US-10-335-207-10	Sequence 10, Appl
39	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
40	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
41	214	73.3	467	10	US-09-759-1308-176	Sequence 176, App
42	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
43	214	73.3	467	16	US-10-741-790-176	Sequence 176, App
44	214	73.3	467	17	US-10-741-600-917	Sequence 917, App
45	214	73.3	467	17	US-10-901-417-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-10-219-329-9

; Sequence 9, Application US/10219329

; Publication No. US20030096757A1

; GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen

; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds

; FILE REFERENCE: 1443.035W01

; CURRENT APPLICATION NUMBER: US/10/219,329

; PRIOR FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: US 10/032,376

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: US 60/312,726

; PRIOR FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 54

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-219-329-9

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Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLKVMPKQPCGVDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 1 MQEFFGLKVTGKPDATLKVMPKQPCGVDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 2

US-10-153-185-9

; Sequence 9, Application US/10153185

; Publication No. US20030148959A1

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
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; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-9

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US-10-219-561-9
; Sequence 9, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Homo sapiens
US-10-219-561-9

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Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 9, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
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; PRIOR APPLICATION NUMBER: 60/312,726
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US-10-032-376A-9

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RESULT 5
US-10-335-207-9
; Sequence 9, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-9

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Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zehrusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
```

```

; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 32
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-32

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Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDATLKVYKQPRCGVDPVAQFVLTEGPRWQTHLTYRIEN 54
Db 50 MQBFFGLKVTGKPDATLKVYKQPRCGVDPVAQFVLTEGPRWQTHLTYRIEN 103

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RESULT 7
US-10-115-479-34
; Sequence 34, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera

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; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 34
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-34

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Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDATLKVYKQPRCGVDPVAQFVLTEGPRWQTHLTYRIEN 54
Db 50 MQBFFGLKVTGKPDATLKVYKQPRCGVDPVAQFVLTEGPRWQTHLTYRIEN 103

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RESULT 8
US-10-115-479-36
; Sequence 36, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera

```

; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Malyanker, Uriel M.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)
 ; CURRENT APPLICATION NUMBER: US/10/115,479
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,687
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/285,325
 ; PRIOR FILING DATE: 2001-04-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 198
 ; SEQ ID NO 36
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVDVAQFVLTEGNPRWEQHLTYRIEN 54
 DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVDVAQFVLTEGNPRWEQHLTYRIEN 103

RESULT 9
 US-10-115-479-38
 ; Sequence 38, Application US/10115479
 ; Publication No. US20040006205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Li
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Zhong, Haihong
 ; APPLICANT: Smithson, Glendda
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Boldog, Ferenc L.;
 ; APPLICANT: Voss, Edward
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: MacDougall, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Mezes, Peter S.
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Malyanker, Uriel M.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)
 ; CURRENT APPLICATION NUMBER: US/10/115,479
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,687
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/285,325
 ; PRIOR FILING DATE: 2001-04-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 198
 ; SEQ ID NO 38
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVDVAQFVLTEGNPRWEQHLTYRIEN 54
 DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVDVAQFVLTEGNPRWEQHLTYRIEN 103

RESULT 10
 US-09-391-104-23
 ; Sequence 23, Application US/09391104
 ; Publication No. US20020031817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Falduto, Michael T.
 ; APPLICANT: Magnuson, Scott R.
 ; APPLICANT: Morgan, Douglas W.
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
 ; TITLE OF INVENTION: OF USING SAME
 ; FILE REFERENCE: 6073.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/391,104
 ; CURRENT FILING DATE: 1999-09-07
 ; PRIOR APPLICATION NUMBER: US 08/814,394
 ; PRIOR FILING DATE: 1997-03-11
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-391-104-23

Query Match 100.0%; Score 292; DB 9; Length 469;

Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 11

US-09-801-196-19
; Sequence 19, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moses, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT FILING DATE: 2001-03-06
; CURRENT APPLICATION NUMBER: US/09/801.196
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-19

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Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 12

US-09-853-386-100
; Sequence 100, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCE: P01972US1
; CURRENT FILING DATE: 2001-05-11
; CURRENT APPLICATION NUMBER: US/09/853.386
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HUMAN
US-09-853-386-100

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 13

US-10-301-822-119
; Sequence 119, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301.822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 119
LENGTH: 469
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-119

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 14

US-10-021-660-76
; Sequence 76, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
CURRENT APPLICATION NUMBER: US/10/021.660
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/09/784.356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 76
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-10-021-660-76

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54

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RESULT 15
US-10-308-279-34
; Sequence 34, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-308-279-34

Query Match      100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPNRWEQTHLTYRIEN 54
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Db      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPNRWEQTHLTYRIEN 120
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Search completed: May 27, 2005, 07:33:59
Job time : 314.308 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 26.7949 seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKNEETLDM.....LTPGNPKWERTNLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	444	1	US-09-178-002-2
2	307	100.0	466	3	US-08-704-711A-17
3	307	100.0	466	3	US-09-521-220-17
4	307	100.0	467	1	US-09-178-002-4
5	307	100.0	467	3	US-09-391-104-24
6	307	100.0	468	3	US-08-448-489-13
7	307	100.0	468	4	US-09-689-730-13
8	221	72.0	469	3	US-08-704-711A-16
9	221	72.0	469	3	US-08-448-489-12
10	221	72.0	469	3	US-09-521-220-16
11	221	72.0	469	3	US-09-391-104-23
12	221	72.0	469	4	US-09-949-016-6223
13	221	72.0	469	4	US-09-689-730-12
14	221	72.0	491	4	US-09-949-016-10875
15	196	63.8	477	3	US-08-704-711A-20
16	196	63.8	477	3	US-08-448-489-15
17	196	63.8	477	3	US-08-281-313-1
18	196	63.8	477	3	US-09-521-220-20
19	196	63.8	477	3	US-09-391-104-21
20	196	63.8	477	4	US-09-689-730-15
21	195	63.5	476	3	US-08-704-711A-21
22	195	63.5	476	3	US-08-448-489-14
23	195	63.5	476	3	US-09-521-220-21
24	195	63.5	476	3	US-09-391-104-22
25	195	63.5	476	4	US-09-949-016-6224
26	195	63.5	476	4	US-09-689-730-14
27	195	63.5	484	4	US-09-949-016-10877

28	188	61.2	471	3	US-09-391-104-25	Sequence 25, Appl
29	188	61.2	480	4	US-09-949-016-10560	Sequence 10560, A
30	179	58.3	471	4	US-08-994-689C-1	Sequence 1, Appl
31	172	56.0	471	4	US-08-994-689C-21	Sequence 21, Appl
32	164	53.4	513	4	US-09-862-631-4	Sequence 4, Appl
33	160	52.1	264	3	US-09-009-156-6	Sequence 6, Appl
34	160	52.1	264	3	US-09-372-154-6	Sequence 6, Appl
35	160	52.1	267	3	US-08-448-489-18	Sequence 18, Appl
36	160	52.1	267	3	US-09-391-104-27	Sequence 27, Appl
37	160	52.1	267	4	US-09-689-730-18	Sequence 27, Appl
38	160	52.1	271	3	US-08-896-062-2	Sequence 2, Appl
39	160	52.1	277	4	US-09-949-016-8131	Sequence 8131, Ap
40	160	52.1	470	3	US-08-068-392-2	Sequence 2, Appl
41	160	52.1	470	3	US-08-396-988-2	Sequence 2, Appl
42	160	52.1	470	3	US-09-391-104-26	Sequence 26, Appl
43	160	52.1	473	4	US-09-949-016-10876	Sequence 10876, A
44	160	52.1	663	4	US-09-194-468A-30	Sequence 30, Appl
45	159	51.8	135	4	US-09-513-999C-4163	Sequence 4163, Ap

ALIGNMENTS

RESULT 1

US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 5.6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGSGFMLTPGNPKWERTNLTIRNY 55

DB 43 MQRFFGLNVTGKNEETLDMKKPRCGVPSGSGFMLTPGNPKWERTNLTIRNY 97

RESULT 2

US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

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Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 55
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RESULT 3
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-MAR-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
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; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-521-220-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 66 MORFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match 100.0%; Score 307; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGNPKWERTNLTIRINY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGNPKWERTNLTIRINY 120

RESULT 6

US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match 100.0%; Score 307; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7

US-09-689-730-13
; Sequence 13, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-13

Query Match 100.0%; Score 307; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGNPKWERTNLTIRINY 55
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RESULT 8

US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-16

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 67 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGNPKWERTNLTIRINY 121

RESULT 9

US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022

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; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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RESULT 10
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
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; FILING DATE: <Unknown>
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; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
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; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

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Best Local Similarity 70.9%; Pred. No. 1.2e-20;
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QY 1 MOREFFGLNVTGKPNBETLDMKKPRCGVDPDSCGFMLTGPNKWKERTNLTIRNY 55
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RESULT 11
US-09-391-104-23
; Sequence 23, Application US/093911104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOREFFGLNVTGKPNBETLDMKKPRCGVDPDSCGFMLTGPNKWKERTNLTIRNY 55
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RESULT 12
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; Sequence 6223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6223
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
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(without alignments)
59.268 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	307	100.0	55	14	US-10-219-561-10
4	307	100.0	55	16	US-10-032-376A-10
5	307	100.0	55	16	US-10-335-207-10
6	307	100.0	467	9	US-09-391-104-24
7	307	100.0	467	9	US-09-801-196-20
8	307	100.0	467	10	US-09-759-130B-176
9	307	100.0	467	14	US-10-131-985-31
10	307	100.0	467	16	US-10-741-790-176
11	307	100.0	467	17	US-10-741-600-917
12	307	100.0	467	17	US-10-901-417-31
13	221	72.0	454	15	US-10-115-479-32

14	221	72.0	454	15	US-10-115-479-34	Sequence 34, Appl
15	221	72.0	454	15	US-10-115-479-36	Sequence 36, Appl
16	221	72.0	454	15	US-10-115-479-38	Sequence 38, Appl
17	221	72.0	469	9	US-09-391-104-23	Sequence 23, Appl
18	221	72.0	469	9	US-09-801-196-19	Sequence 19, Appl
19	221	72.0	469	9	US-09-853-386-100	Sequence 100, Appl
20	221	72.0	469	14	US-10-301-822-119	Sequence 119, Appl
21	221	72.0	469	14	US-10-021-660-76	Sequence 76, Appl
22	221	72.0	469	14	US-10-308-279-34	Sequence 34, Appl
23	221	72.0	469	14	US-10-131-985-23	Sequence 23, Appl
24	221	72.0	469	15	US-10-295-027-12	Sequence 12, Appl
25	221	72.0	469	15	US-10-295-027-14	Sequence 14, Appl
26	221	72.0	469	15	US-10-295-027-1167	Sequence 1167, Appl
27	221	72.0	469	15	US-10-295-027-1168	Sequence 1168, Appl
28	221	72.0	469	15	US-10-115-479-30	Sequence 30, Appl
29	221	72.0	469	15	US-10-115-479-40	Sequence 40, Appl
30	221	72.0	469	15	US-10-211-462-22	Sequence 22, Appl
31	221	72.0	469	15	US-10-188-832-6	Sequence 6, Appl
32	221	72.0	469	16	US-10-734-564-109	Sequence 109, Appl
33	221	72.0	469	17	US-10-901-417-23	Sequence 23, Appl
34	221	72.0	470	15	US-10-447-315-1	Sequence 1, Appl
35	221	72.0	496	14	US-10-106-698-6283	Sequence 6283, Appl
36	214	69.7	54	14	US-10-219-329-9	Sequence 9, Appl
37	214	69.7	54	14	US-10-153-185-9	Sequence 9, Appl
38	214	69.7	54	14	US-10-219-561-9	Sequence 9, Appl
39	214	69.7	54	16	US-10-032-376A-9	Sequence 9, Appl
40	214	69.7	54	16	US-10-335-207-9	Sequence 9, Appl
41	198	64.5	173	15	US-10-115-479-48	Sequence 48, Appl
42	196	63.8	267	14	US-10-133-797-73	Sequence 73, Appl
43	196	63.8	477	9	US-09-391-104-21	Sequence 21, Appl
44	196	63.8	477	9	US-09-801-196-24	Sequence 24, Appl
45	196	63.8	477	14	US-10-171-311-137	Sequence 137, Appl

ALIGNMENTS

RESULT 1

US-10-219-329-10
; Sequence 10, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443 035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-10

Query Match 100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSCGGFMTGPNPKWERTNLTIRNY 55

Db 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSCGGFMTGPNPKWERTNLTIRNY 55

RESULT 2

US-10-153-185-10
; Sequence 10, Application US/10153185
; Publication No. US20030148959A1

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-10

Query Match          100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||
Db 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||

RESULT 3
US-10-219-561-10
; Sequence 10, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-10

Query Match          100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||
Db 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||

RESULT 4
US-10-032-376A-10
; Sequence 10, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
```

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; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-10

Query Match          100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||
Db 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||

RESULT 5
US-10-335-207-10
; Sequence 10, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-10

Query Match          100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||
Db 1 MORFFGLNVTKPNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
   |||||||

RESULT 6
US-09-391-104-24
; Sequence 24, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match          100.0%; Score 307; DB 9; Length 467;
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Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 7
US-09-801-196-20
; Sequence 20, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moes, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801.196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-20

Query Match 100.0%; Score 307; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 8
US-09-759-130B-176
; Sequence 176, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: US85.
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09/759.130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-05-24
; PRIOR FILING DATE: 1999-06-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364

Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 9
US-10-131-985-31
; Sequence 31, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131.985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726.295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-31

Query Match 100.0%; Score 307; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 10
US-10-741-790-176
; Sequence 176, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J

```

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; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USBS
; FILE REFERENCE: MP100-535OMNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 11
US-10-741-600-917
; Sequence 917, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 7397
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-917

Query Match 100.0%; Score 307; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 12
US-10-901-417-31
; Sequence 31, Application US/10901417
; Publication No. US20050026936A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-417-31

Query Match 100.0%; Score 307; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 13
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyancker, Uriel M.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.

```



```

; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 32
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-32

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Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTVIRNY 55
Db 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 104

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```

RESULT 14
US-10-115-479-34
; Sequence 34, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.

```

```

; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 34
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-34

```

```

Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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```

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTVIRNY 55
Db 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 104

```

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RESULT 15
US-10-115-479-36
; Sequence 36, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
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; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.

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; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 36
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-36

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Query Match      72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 MORFFGLNTGKPNETHDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRIY 55
Db      50 MQEFFFGLKVTGRDAETLKMVKQPRCGVDPVAQFVLTEGNPRWEQTHLTYYRIY 104

```

Search completed: May 27, 2005, 07:34:00
Job time : 321.128 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 106.827 Seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGRPNSTLDM.....LTPGNPKWERTNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	55	6	ABP97132 Human mat
2	307	100.0	55	6	ABG76318 Human mat
3	307	100.0	55	8	ADQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AAB84610 Amino aci
6	307	100.0	467	4	AAB84610 Amino aci
7	307	100.0	467	4	AAG65358 Human neu
8	307	100.0	467	6	AAB32581 Secreted
9	307	100.0	467	8	ADQ10212 Human pol
10	307	100.0	467	8	ADQ39254 Human myo
11	226	73.6	454	8	ADL33947 Human G-c
12	221	72.0	454	7	ADE16002 G-coupled
13	221	72.0	454	7	ADE16004 G-coupled
14	221	72.0	454	7	ADE16008 G-coupled
15	221	72.0	454	7	ADE16006 G-coupled
16	221	72.0	454	8	ADL33945 Human G-c
17	221	72.0	454	8	ADL33943 Human G-c
18	221	72.0	455	8	ADL33941 Human G-c
19	221	72.0	469	4	AAB84606 Amino aci
20	221	72.0	469	4	AAB10415 Human mat
21	221	72.0	469	6	ABU03466 Angiogene
22	221	72.0	469	6	ABR58543 Human can
23	221	72.0	469	6	ABR58542 Human can
24	221	72.0	469	6	ABR48148 Human bla
25	221	72.0	469	6	ABU56596 Lung canc

ALIGNMENTS

RESULT 1

ABP97132

ID ABP97132 standard; peptide; 55 AA.

XX AC ABP97132;

XX DT 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

XX KW Human, matrix metalloproteinase; MMP; anticancer; wound healing;

XX KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;

XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;

XX KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;

XX KW dermatological; metastatic; non-metastatic; vascularised; heart disease;

XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;

XX KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX XX WO2003018748-A2.

XX XX 06-MAR-2003.

XX XX 15-AUG-2002; 2002WO-US026319.

XX XX 16-AUG-2001; 2001US-0312726P.

XX XX 21-DEC-2001; 2001US-00032376.

XX XX 21-MAY-2002; 2002US-00153185.

XX XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX XX Quirk S, Weart IP;

XX XX WPI; 2003-391408/36.

XX XX Anti-angiogenic composition comprising peptide inhibitor of matrix

XX XX metalloproteinase, useful for decreasing the expression of vascular

XX XX endothelial growth factor and treating cancers and tissue injuries.

XX XX Claim 17; Page 16; 103pp; English.

XX XX The present invention describes an anti-angiogenic composition (I) for

XX XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)

XX XX comprises an effective amount of a peptide inhibitor of matrix

XX XX metalloproteinase (MMP), where the peptide can inhibit the expression of

XX XX VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective,

XX XX antidiabetic, ophthalmological and dermatological activities. (I) can be

Abu56597 Lung canc
Abu07454 Protein d
Abp54454 Matrix me
Adb79176 Matrix me
Ade34550 Human eki
Ade16000 G-coupled
Ade16010 G-coupled
Adn39849 Cancer/an
Adn38694 Cancer/an
Adn38696 Cancer/an
Adn39850 Cancer/an
Adn95538 Human BEC
Adl93949 Human G-c
Adl93939 Human G-c
Adq29683 Human col
Adsl9177 Human mat
Adn07695 Human mat
Ade07892 Novel pro
Aag75509 Human col
Aap93628 Sequence

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55

RESULT 2
 ABG76318
 ID ABG76318 standard; protein; 55 AA.
 XX
 AC ABG76318;

DT 10-MAY-2003 (first entry)
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #10.

XX Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.
 XX
 OS Homo sapiens.

XX WO2003016520-A1.
 PN 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.
 XX 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA Quirk S, Malik S, Villanueva JM;
 PI WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating and preventing scarring, improving skin tone,
 CC reducing wrinkling and for simulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;
 Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55

RESULT 3
 ADQ17093
 ID ADQ17093 standard; peptide; 55 AA.
 XX
 AC ADQ17093;

XX 23-SEP-2004 (first entry)
 DE Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.
 OS US2004127421-A1.
 PN 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.
 XX 30-DEC-2002; 2002US-00335207.

XX (WALT/) MALIK S.
 PA (QUIR/) QUIRK S.
 XX Malik S, Quirk S;
 PI WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 10; 60pp; English.
 XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 55 AA;
 Query Match 100.0%; Score 307; DB 8; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTIRINY 55

RESULT 4
 AAG65357
 ID AAG65357 standard; protein; 444 AA.
 XX
 AC AAG65357;

XX 30-NOV-2001 (first entry)
 DT

DE Human MMP-8alt polypeptide.

XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
 XX anti-arthritis; cytoskeletal; anti-Parkinsonian; neuroprotective;
 KW nontropic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
 KW Huntington's disease; human; splice variant.
 XX Homo sapiens.

XX US1973-H.

XX 03-JUL-2001.

XX 22-OCT-1998; 98US-00178002.

XX 22-OCT-1998; 98US-00178002.

XX (NOVS) NOVARTIS AG.

XX Hu S;

XX WPI: 2001-431511/46.

XX N-PSDB; AAH47515.

XX New MMP-8alt polynucleotides and polypeptides useful as research reagents
 PT and materials for discovering treatments and diagnostics to human
 PT disease, or as targets for identifying inhibitors of MMP-8alt expression.

XX Claim 11; Col 25-30; 25pp; English.

XX The invention relates to human MMP-8alt polypeptide and polynucleotides.
 CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)
 CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant
 CC methodology. The polynucleotides and polypeptides may be used as research
 CC reagents and materials for the discovery of treatments and diagnostics to
 CC human disease, and as targets for identifying modulators. Inhibitors of
 CC MMP-8alt polynucleotide or polypeptide expression may be used to treat
 CC and/or prevent arthritis, cancer and cancer metastasis, and diseases
 CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's
 CC disease and Huntington's disease. The present sequence represents the
 CC human MMP-8alt polypeptide

XX SQ Sequence 444 AA;

Query Match 100.0%; Score 307; DB 4; Length 444;
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGNPKWERTNLTIRNY 55
 |||||
 Db 43 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGNPKWERTNLTIRNY 97
 |||||

RESULT 5
 AAB84610
 ID AAB84610 standard; protein; 467 AA.
 XX AAB84610;
 XX 05-SEP-2001 (first entry)

XX Amino acid sequence of matrix metalloproteinase-8.

XX Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound.
 XX Homo sapiens.

XX WO200149309-A2.

XX 12-JUL-2001.

XX 21-DEC-2000; 2000WO-1B001935.

XX 29-DEC-1999; 99GB-00030768.

XX (PFIZ) PFIZER LTD.

XX (PFIZ) PFIZER INC.

XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
 WPI: 2001-418351/44.
 XX N-PSDB; AAH28225.

XX Composition for the treatment of damaged tissue i.e. chronic wounds and
 PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 PT factor.

XX Disclosure; Page 555; 572pp; English.

XX The specification describes a pharmaceutical composition, comprising a
 CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
 CC inhibits the action of at least one specific adverse protein, i.e. a
 CC protease, that is upregulated in a damaged tissue such as a wound
 CC environment. Growth factors which are included in the composition of the
 CC invention are platelet-derived growth factor (PDGF), fibroblast growth
 CC factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
 CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
 CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
 CC and chrysalin. Inhibitors which are included in the composition of the
 CC invention include inhibitors of urokinase-type plasminogen activator
 CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
 CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
 CC The present sequence represents a human MMP-8, and is used to produce the
 CC composition of the invention

XX SQ Sequence 467 AA;

Query Match 100.0%; Score 307; DB 4; Length 467;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGNPKWERTNLTIRNY 55
 |||||
 Db 66 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGNPKWERTNLTIRNY 120
 |||||

RESULT 6
 AAE10416
 ID AAE10416 standard; protein; 467 AA.
 XX AAE10416;
 XX 10-DEC-2001 (first entry)

XX Human matrix metalloproteinase-8 (MMP-8) protein.

XX Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;
 KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..20 /label= Signal_peptide
 FT Protein 21..467 /label= Mature_MMP_8_protein
 FT Domain 89..95 /label= Cysteine_switch_domain
 FT


```
PA (FRASER) FRASER C C.
PA (BARN) BARNES T M.
PA (SHAR) SHARP J D.
PA (KIRS) KIRST S J.
PA (MYER) MYERS P S.
PA (LEIB) LEIBY K R.
PA (HOLT) HOLTZMAN D A.
PA (MCCA) MCCARTHY S A.
PA (WRIG) WRIGHTON N.
PA (MACK) MACKAY C R.
PA (GOOD) GOODEARL A D J.
XX
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
PI
XX WPI: 2003-456290/43.
XX N-PSDB; ACD66741.
XX
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.
XX
XX Disclosure; Fig 15V-15W; 482pp; English.
XX
XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related protein of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 467 AA;
SQ
Query Match 100.0%; Score 307; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRYNY 55
DB 66 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRYNY 120
RESULT 9
ADQ10212
ID ADQ10212 standard; protein; 467 AA.
XX
XX ADQ10212;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human polypeptide #75.
DE
XX
XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;
XX anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;
XX hypoadenism; cardiovascular disorder; arthritis; osteoarthritis;
XX atherosclerosis; hypertension; bacterial infection; psoriasis;
XX diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
XX Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;
XX goiter; infertility; endometriosis; muscular disorder.
XX
```

```
OS Homo sapiens.
XX
XX US2004121396-A1.
XX
XX 24-JUN-2004.
XX
XX 19-DEC-2003; 2003US-00741790.
XX
XX 14-JUN-1999; 99US-00333159.
XX 29-JUN-1999; 99US-00342364.
XX 10-SEP-1999; 99US-00393996.
XX 19-OCT-1999; 99US-00420707.
XX 07-JAN-2000; 2000US-00479249.
XX 27-APR-2000; 2000US-00559497.
XX 24-MAY-2000; 2000US-00578063.
XX 16-JUN-2000; 2000US-00596194.
XX 23-JUN-2000; 2000US-00602871.
XX 30-JUN-2000; 2000US-00608452.
XX 12-JAN-2001; 2001US-00759130.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
PI
XX WPI: 2004-479675/45.
XX
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypoadenism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, goiter, infertility.
XX
XX Disclosure; SEQ ID NO 176; 483pp; English.
XX
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a
CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypoadenism,
CC cardiovascular disorders, arthritis, osteoarthritis, atherosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polypeptide of the invention. Note: The sequence data
CC for this patent did not form part of the invention. Note: The sequence data
CC obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX Sequence 467 AA;
SQ
Query Match 100.0%; Score 307; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRYNY 55
DB 66 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRYNY 120
RESULT 10
ADQ39254
ID ADQ39254 standard; protein; 467 AA.
XX
XX ADQ39254;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
```

DE	Human myocardial infarction-associated gene derived protein, SEQ ID 917.
XX	
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW	cardiac; gene therapy; human.
OS	Homo sapiens.
XX	
PN	WO2004058052-A2.
XX	
PD	15-JUL-2004.
XX	
PF	22-DEC-2003; 2003WO-US040978.
XX	
PR	20-DEC-2002; 2002US-0434778P.
PR	10-MAR-2003; 2003US-0453135P.
PR	30-APR-2003; 2003US-0466412P.
PR	23-SEP-2003; 2003US-0504955P.
XX	
PA	(APPL-) APPLERA CORP.
XX	
PI	Cargill M, Devlin JJ, Iakoubova O;
XX	
DR	WPI; 2004-533949/51.
DR	N-PSDB; ADQ38426.
XX	
PT	Identifying an individual who has an altered risk for developing
PT	myocardial infarction by detecting a single nucleotide polymorphism in
PT	the individual's nucleic acids.
XX	
PS	Claim 10; SEQ ID NO 917; 145pp; English.
XX	
CC	The invention relates to a novel method for identifying an individual who
CC	has an altered risk for developing myocardial infarction. The method
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC	the nucleotide sequences given in the specification in the individual's
CC	nucleic acids, where the presence of the SNP is correlated with an
CC	altered risk for myocardial infarction in the individual. The invention
CC	further comprises: an isolated nucleic acid molecule comprising at least
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC	the specification or its complement and encoding any one of the amino
CC	acid sequences given in the specification; an isolated polypeptide
CC	comprising an amino acid sequence given in the specification; an antibody
CC	that specifically binds to the polypeptide or its antigen-binding
CC	fragment; an amplified polynucleotide containing an SNP given in the
CC	specification and which is between about 16 and 1000 nucleotides in
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC	method for identifying an agent useful in treating or preventing
CC	myocardial infarction. The novel detection method has cardiac activity.
CC	The nucleic acids of the invention may be used in gene therapy. The
CC	method is useful in identifying an individual who has an increased or
CC	decreased risk for developing myocardial infarction and for preparing a
CC	composition for treating or preventing myocardial infarction. This
CC	sequence represents the protein of a human myocardial infarction-
CC	associated gene containing one or more SNPs of the invention. Note: This
CC	sequence was not shown in the specification. The sequence has come from
CC	an electronic sequence listing downloaded from the WIPO website.
XX	
SQ	Sequence 467 AA;
	Query Match 100.0%; Score 307; DB 8; Length 467;
	Best Local Similarity 100.0%; Pred. No. 4.9e-33;
	Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MORFFGLNVTGKPNBETLDMKKPCGVPDGGGFMFTGPNPKWERTNLTRYNY 55
DB	66 MORFFGLNVTGKPNBETLDMKKPCGVPDGGGFMFTGPNPKWERTNLTRYNY 120
RESULT 11	
ADL93947	ADL93947 standard; protein: 454 AA.


```

PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CM, Macdougall JR, Rastelli L, Anderson DW;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger S, Mazur A;
XX
DR WPI; 2004-224146/21.
DR N-PSDB; ADL93946.
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
PS Claim 1; Page 69; 220pp; English.
XX
CC The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, atrial septal defect,
CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
CC subaortic stenosis, ventricular septal defect, valve diseases, tubercous
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, neoplasm,
CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
SQ Sequence 454 AA;

Query Match 73.6%; Score 226; DB 8; Length 454;
Best Local Similarity 72.7%; Pred. No. 6.3e-22;
Matches 40; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTYSRIY 55
DB ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
50 MQEFGKVTGKDAETLKWKPRCGVDPVQAQFVLTEGNPRWEQNTLTYSRIY 104

RESULT 12
ADE16002
ID ADE16002 standard; protein; 454 AA.
XX
AC ADE16002;
XX
XX 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID No 32.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nontropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaeimic; neuroprotective;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX

```

Query Match

72.0%; Score 221; DB 7; Length 454;

Sequence 454 AA;

Best Local Similarity 70.9%; Pred. No. 3.1e-21; Mismatches 7; Indels 0; Gaps 0;
Matches 39; Conservative

QY 1 MQRFTGLNVTGKPNBETLDMKKPCRGVDPDGGFMLTGPCNPKWERTNLTVIRNY 55
DB 50 MQEFFGLKVTGKPDATLTKVMKQPCRGVDPDVAQFVLTEGNPRWEQHLTYRIENY 104

RESULT 13
ADE16004
ID ADE16004 standard; protein; 454 AA.
XX ADE16004;
XX
DT 29-JAN-2004 (first entry)
DE G-coupled protein receptor related polypeptide, SEQ ID NO 34.
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW viricide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX Homo sapiens.
OS
XX
PN WO200283841-A2.
PD
XX 24-OCT-2002.
PF 03-APR-2002; 2002WO-US010713.
XX 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282334P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0284210P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena EA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
XX WPI; 2003-067574/06.
DR N-PSDB; ADE16003.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 34; 320pp; English.

XX The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC viricide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
SQ Sequence 454 AA;
Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 3.1e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFTGLNVTGKPNBETLDMKKPCRGVDPDGGFMLTGPCNPKWERTNLTVIRNY 55
DB 50 MQEFFGLKVTGKPDATLTKVMKQPCRGVDPDVAQFVLTEGNPRWEQHLTYRIENY 104

RESULT 14
ADE16008
ID ADE16008 standard; protein; 454 AA.
XX ADE16008;
XX
DT 29-JAN-2004 (first entry)
DE G-coupled protein receptor related polypeptide, SEQ ID NO 38.
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW viricide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX Homo sapiens.
OS
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX
XX 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282334P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.
PR 13-APR-2001; 2001US-0284210P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
XX
XX

PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0286068P.
 PR 24-APR-2001; 2001US-0286213P.
 PR 27-APR-2001; 2001US-0286509P.
 PR 30-MAY-2001; 2001US-0286850P.
 PR 31-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX (CURA-) CURAGEN CORP.
 XX
 PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16007.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 FT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 FT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 38; 320pp; English.
 XX
 CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
 Best Local Similarity 70.9%; Pred. No. 3.1e-21;
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQBFGLVTKGNEETLDMKKPCRGVDPDGGFMLTPGNPKWERTNLTTRIYNY 55
 DB 50 MQBFFGLKVTGKPDATFLKVMKQPCRGVDPDVAQFVLTEGPNRWEQTLTRIYNY 104

RESULT 15
 ADE16006
 ID ADE16006 standard; protein; 454 AA.
 XX
 AC ADE16006;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE G-coupled protein receptor related polypeptide, SEQ ID NO 36.
 XX
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200283841-A2.
 PN
 XX
 PD 24-OCT-2002.
 XX
 PF 03-APR-2002; 2002MO-US010713.
 XX
 XX 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16005.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 FT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 FT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 36; 320pp; English.
 XX
 CC The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

CC antiparkinsonian, haemostatic, and antilipaemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
XX polypeptides of the invention.
SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 3.1e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNPKWERTNLTVIRNY 55
DB 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVQAQVLTGPNRWEQHLTYRIENY 104

Search completed: May 27, 2005, 06:52:55
Job time : 106.827 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 20.8013 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKPEETLDM.....LTPGNPKWERTNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collage
2	233	75.9	468	1 KCRBI	interstitial colla
3	231	75.2	469	1 KCPGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCB0I	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 JC6505	stromelysin 2 (EC
10	193	62.9	477	1 KCMSS1	stromelysin 1 (EC
11	192	62.5	478	1 KCRBS1	stromelysin 1 (EC
12	190	61.9	476	1 KCRTS2	stromelysin 2 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KCRTHH	stromelysin 1 (EC
17	183	59.6	483	2 JC5743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	metalloelastase HM
21	160	52.1	663	1 S46492	gelatinase A (EC 3
22	155	50.5	662	2 S70365	gelatinase A (EC 3
23	153	49.8	660	1 A28153	gelatinase A (EC 3
24	153	49.8	662	2 A42496	gelatinase A (EC 3
25	153	49.8	662	2 S34780	gelatinase A (EC 3
26	139.5	45.4	669	2 I38029	matrix metalloprot
27	138	45.0	462	2 A42401	macrophage elastas
28	134.5	43.8	582	2 I38028	matrix metalloprot
29	134.5	43.8	582	2 I84471	matrix metalloprot

RESULT 1

KCHUN

neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human

N;Alternate names: matrix metalloproteinase 8

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C;Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32527; S62

R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Steve

J. Biol. Chem. 285, 11421-11424, 1990

A;Title: Human neutrophil collagenase. A distinct gene product with homology to other ma

A;Reference number: A37073; MUID:90307647; PMID:2164002

A;Accession: A37073

A;Molecule type: mRNA

A;Residues: 1-467 <HNS>

A;Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G180618

R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.

Blood 77, 2731-2738, 1991

A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.

A;Reference number: A61175; MUID:91255696; PMID:1646048

A;Accession: A61175

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-31,'I',33-86,'E',88-467 <DEV>

A;Accession: B61175

A;Molecule type: protein

A;Residues: 263-264,'X',272-273,'X',275,'X',277 <DE2>

R;Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V

Biochemistry 29, 10628-10634, 1990

A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with

A;Reference number: A36230; MUID:91104978; PMID:2176876

A;Accession: A36230

A;Molecule type: protein

A;Residues: 'X',86-87,'X',89-90,'X',92-97,'X',99-111,'X',113-120 <MAL>

R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 189, 295-300, 1990

A;Title: Characterization and activation of procollagenase from human polymorphonuclear

A;Reference number: S09680; MUID:90249372; PMID:2159879

A;Accession: S09680

A;Molecule type: protein

A;Residues: 21-31,'I',33-39,'I',41-47,'V',49-53,'I',55-72,'G',74-86,'E',88-111,'X',113-1

R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Biol. Chem. Hoppe-Seyler 371, 733, 1990

A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.

A;Reference number: S11026; MUID:91000455; PMID:2169766

A;Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990

A;Accession: S11026

A;Molecule type: protein

A;Residues: 21-31,'I',33-53,'I',55-72,'G',74-111,'X',113-140:183-203,'X',205-209:248-261

A;Note: 87-Glu was also found

R;Blaeser, J.; Knaeuper, V.; Oesthus, A.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 202, 1223-1230, 1991

A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
A;Reference number: S19576; MUID:92111500; PMID:1662606
A;Accession: S19576
A;Molecule type: protein
A;Residues: 69-103 <BL2>
R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.
FEBS Lett. 313, 59-61, 1992
A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.
A;Reference number: S27225; MUID:93050220; PMID:1330697
A;Accession: S27225
A;Molecule type: protein
A;Residues: 68-103 <BLA>
R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.
Biochem. J. 291, 847-854, 1993
A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
A;Reference number: S32527; MUID:93256897; PMID:8489511
A;Accession: S32527
A;Molecule type: protein
A;Residues: 100-112;263-276 <KN3>
R;Knaeuper, V.; Murphy, G.; Tschesche, H.
Eur. J. Biochem. 235, 187-191, 1996
A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
A;Reference number: S62608; MUID:96202934; PMID:8631328
A;Accession: S62608
A;Molecule type: protein
A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A67078; PDB:1MNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 119-123, 1994
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, Nat. Struct. Biol. 1, 119-123, 1994
A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.
A;Reference number: A58274; MUID:95384762; PMID:7656015
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 119-123, 1994
C;Comment: This protein is more highly glycosylated than interstitial collagenase and is C;Genetics:
A;Gene: GDB:MMP8; CLG1
A;Cross-references: GDB:128173; OMIM:120355
A;Map position: 11q22.2-11q22.3
C;Function:
A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous A;Note: Cleaves type I collagen most rapidly
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein F;1-20/Domain: signal sequence #status predicted <SIG>
C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; i F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-467/Product: procollagenase #status predicted <PRO>
F;21-100/Domain: activation peptide #status experimental
F;59-262/Domain: matrix metalloproteinase homology <ACT>
F;89-96/Region: autoinhibitory
F;101-467/Product: neutrophil collagenase #status predicted <MAT>
F;273-464/Domain: hemopexin repeat homology <PXN>
F;54,73,112,119,204,246/Binding site: carboxylate (Asn) (covalent) #status predicted
F;73-74/Cleavage site: Asn-Val (autolytic) #status experimental
F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental
F;167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime F;174,175,177,179,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e F;217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental
F;218/Active site: Glu #status predicted
F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental
F;279-464/Disulfide bonds: #status predicted

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

RESULT 2

KCRBI

interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue coll
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
A;Accession: A27500; B27500; I46694
R;Finii, M.E.; Plucinska, I.M.; Mayer, A.S.; Grosse, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprotei
A;Reference number: A27500; MUID:88077876; PMID:2825772
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <PIN>
A;Cross-references: UNIPROT:P13943; GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391;399-468 <F12>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finii, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerhof
Coll. Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial
A;Reference number: I46694; MUID:87029174; PMID:3021384
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <F13>
A;Cross-references: GB:M25663; NID:G531211; PID:G531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
C;Comment: Procollagenase can be activated without removal of the activation peptide. Str
tion peptide by other proteinases
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whic
C;Genetics:
A;Introns: 34/3; 116/2; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteir
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-468/Product: procollagenase #status predicted <PRO>
F;19-98/Domain: activation peptide #status predicted <ACT>
F;59-96/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status i
F;119,142/Binding site: carboxylate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 1.6e-21;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 MORFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
Db 66 MOEPPGLKVTGKPDATLKMKKPRCGVDPVAQFVLTFGNPRWEQTHLTIRNY 120

RESULT 3

KCPGI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue coll
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
A;Accession: S15986; S13597
R;Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of e
A;Reference number: S15986; MUID:91333421; PMID:1651440
A;Accession: S15986

tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are found in the extracellular matrix.
C:Genetics:
A:Gene: GDB:MMP1; CLG
A:Cross-references: GDB:119783; OMIM:120353
A:Map position: 11q22.2-11q22.3
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status experimental <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status experimental <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F:278-466/Disulfide bonds: #status experimental

Query Match 72.0%; Score 221; DB 1; Length 469;
Best Local Similarity 70.9%; Pred. No. 5.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQRPFGLVTKGNEETLDMKKPCRCVPSGGFMLTPGNPKWERNLTVIRNY 55
Db 67 MQSFFGLKVGKPDATLTKVKKPCRCVPSGGFMLTPGNPKWERNLTVIRNY 121

RESULT 5
KCB01
Interstitial collagenase (EC 3.4.24.7) precursor - bovine
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S14654; S20336; S14655
R:Tamura, M.; Shmookawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991
A:Reference number: S14654
A:Accession: S14654
A:Molecule type: mRNA
A:Residues: 1-469 <MAT>
A:Cross-references: UNIPROT:P28053; EMBL:X58256; NID:9259; PIDN:CAA41210.1; PID:g260
R:Stuckey, B.D.; Jeffrey, J.J.; Weigus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A:Title: Purification and characterization of bovine interstitial collagenase and tissue collagenase
A:Reference number: S20336; MUID:92161820; PMID:1311165
A:Accession: S20336
A:Molecule type: protein
A:Residues: 19-21, 'PP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125 <ACT>
C:Comment: Procollagenase can be activated without removal of the activation peptide. Substrate specificity is determined by the activation peptide.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are found in the extracellular matrix.
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-469/Product: procollagenase #status predicted <PRO>
F:19-99/Domain: activation peptide #status predicted <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted

F:278-466/Disulfide bonds: #status predicted

Query Match 71.0%; Score 218; DB 1; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.3e-19;
Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MORPFGLVNTGKPNSETLDMKMKPCRGVDPDGGFMLTPGNPKWERTNLTVIRNY 55
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 67 MQKPFGLRVTKPDATLNMVKQPCRGVDPDVPFVLTPGKSCWENTLTIRIENY 121
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
151267
collagenase (EC 3.4.24.-) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: 151267
R:Oofusa, K.; Yomori, S.; Yoshizato, K.
Int. J. Dev. Biol. 38, 345-350, 1994
A:Title: Regionally and hormonally regulated expression of genes of collagen and collagenase
A:Reference number: 151267; MUID:95071832; PMID:7981043
A:Accession: 151267
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-384 <OOF>
A:Cross-references: UNIPROT:Q11133; GB:S75623; NID:G913070; PIDN:AA32661.1; PID:G913071
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:53-231/Domain: matrix metalloproteinase homology <MMP>
F:236-381/Domain: hemopexin repeat homology <PN>
F:81,189,193/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
F:190/Active site: Glu #status predicted

Query Match 65.6%; Score 201.5; DB 2; Length 384;
Best Local Similarity 65.5%; Pred. No. 1.2e-17;
Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MORPFGLVNTGKPNSETLDMKMKPCRGVDPDGGFMLTPGNPKWERTNLTVIRNY 55
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 57 LKQFFGLVTKPDATLNMVKQPCRGVDPDVGVEVLTGPNRWENTHLYRIENY 110
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
KCHUS1
stromelysin 1 (EC 3.4.24.17) precursor [validated] - human
N:Alternate names: angiotatin-converting enzyme; collagenase activating protein; matrix
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: A28156; A28399; A60964; S15427
R:Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.
J. Biol. Chem. 263, 6742-6745, 1988
A:Title: The complete primary structure of human matrix metalloproteinase-3. Identity with
A:Reference number: A28156; MUID:88198243; PMID:3360803
A:Accession: A28156
A:Molecule type: mRNA
A:Residues: 1-44, 'E', '46-477 <SAU>
A:Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G188619
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rammedorf, H.J.; Smith, B.J.; Lyons, A.; Harris,
Biochem. J. 240, 913-916, 1986
A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A:Reference number: A30336; MUID:87156645; PMID:3030290
A:Accession: C29157
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-477 <WHI>
A:Cross-references: EMBL:X05232; NID:G36632; PIDN:CAA28859.1; PID:G36633
R:Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eilsen, A.Z.; Marmer, B.L.; Grant, G.A.;
Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987
A:Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specificity
A:Reference number: A28399; MUID:88016164; PMID:3477804
A:Accession: A28399
A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-49, 'G', 51-419, 'L', 421-477 <WIL>
A:Cross-references: GB:U78045; NID:g1689257; PIDN:AAB36942.1.; PID:g1688259
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed by R:Lark, M.W.; Walakowits, L.A.; Shah, T.K.; Vanniddlesworth, J.; Cameron, P.M.; Lin, T.Y. Connect. Tissue Res. 25, 49-65, 1990
A:Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A:Reference number: A60964; MUID:91059606; PMID:2173990
A:Accession: A60964
A:Molecule type: protein
A:Residues: 18-29;100-108 <LAR>
R:Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.
Biochem. J. 276, 217-221, 1991
A:Title: Purification of recombinant human prostromelysin. Studies on heat activation to
A:Reference number: S15427; MUID:91248150; PMID:2039471
A:Accession: S15427
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-23 <Bio>
R:Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
A:Reference number: A58812; MUID:9548733; PMID:9548733
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February 1997
A:Reference number: A68466; PDB:1HFS
A:Contents: annotation: X-ray crystallography, 1.70 angstroms, residues 105-160
R:Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.
Protein Sci. 4, 1966-1976, 1995
A:Title: Stromelysin-1: three-dimensional structural structure of the inhibited catalytic domain an
A:Reference number: A58814; MUID:96117647; PMID:8535233
A:Contents: annotation: X-ray crystallography, 1.70 angstroms
R:Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.
Biochemistry 30, 6476-6483, 1991
A:Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch
A:Reference number: A39589; MUID:91274298; PMID:1647201
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1995
A:Reference number: A66637; PDB:1SLM
A:Contents: annotation: X-ray crystallography, 1.90 angstroms, residues 33-47;57-267
R:Gooley, P.R.; O'connell, J.F.
submitted to the Brookhaven Protein Data Bank, March 1995
A:Reference number: A67284; PDB:2SRT
A:Contents: annotation: conformation by (1)H-NMR, residues 100-272
R:Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Ess
Biochemistry 32, 13098-14008, 1993
A:Title: Secondary structure and zinc ligation of human recombinant short-form stromelys
A:Reference number: A58815; MUID:94059987; PMID:8241164
A:Contents: annotation: conformation by (1)H-NMR
C:Comment: Stromelysin 1 activates ice proenzyme after cleavage(s) within the activation
C:Comment: Prostromelysin 1 is found in glycosylated and unglycosylated forms, both of whi
C:Genetics:
A:Gene: GDB:MMP3; STWY; STWY1
A:Cross-references: GDB:120727; OMIM:185250
A:Map position: 11q23-11q23
C:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
A:Note: Degrades various extracellular matrix proteins, including fibronectin, plasminoge
Plasminogen to yield a fragment with angiotensin activity
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-477/Product: prostromelysin 1 #status experimental <PRO>
F;18-99/Domain: activation peptide #status experimental <ACT>
F;60-264/Domain: matrix metalloproteinase homology <MMP>
F;100-477/Product: stromelysin 1 #status experimental <MAT>
F;284-477/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;120/Binding site: carboxylate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-477/Product: prostromelysin 1 #status predicted <PRO>
F:18-99/Domain: activation peptide #status predicted <ACT>
F:60-264/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-477/Product: stromelysin 1 #status predicted <MAT>
F:284-477/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:218,222,228/binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:290-477/Disulfide bonds: #status predicted

Query Match 62.5%; Score 193; DB 1; Length 477;
Best Local Similarity 58.2%; Pred. No. 1.9e-16;
Matches 32; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTKPNEETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRINY 55
Db 67 MQKFLGLEMTGKLDNSTWELMHKPCRGVDSGGFSTFGSPKWRKSHITIRINY 121

RESULT 11

KCRBS1

stromelysin 1 (EC 3.4.24.17) precursor - rabbit
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro-
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A37306; A29157
R:Finai, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff, C.
Arthritis Rheum. 30, 1254-1264, 1987
A:Title: Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase tha
ed with collagenase.
A:Reference number: A37306; MUID:88077214; PMID:2825726
A:Accession: A37306
A:Molecule type: mRNA
A:Residues: 1-478 <FIN>
R:Cross-references: UNIPROT:P28863; GB:M25664; NID:G165709; PIDN:AAA31467.1; PID:G165710
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,
Biochem. J. 240, 913-916, 1986
A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A:Reference number: A90336; MUID:87156645; PMID:3030290
A:Accession: A29157
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-82,'D','84'-127,'K','129'-167,'GNS' <WHI>
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of whi
C:Function:

A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallopro
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-478/Product: prostromelysin 1 #status predicted <PRO>
F:18-100/Domain: activation peptide #status predicted <ACT>
F:61-265/Domain: matrix metalloproteinase homology <MMP>
F:91-98/Region: autoinhibitory
F:101-478/Product: stromelysin 1 #status predicted <MAT>
F:285-478/Domain: hemopexin repeat homology <PXN>
F:93,219,223,229/binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:121/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:219,223,229/binding site: zinc, catalytic (His) (active) #status predicted
F:220/Active site: Glu #status predicted
F:291-478/Disulfide bonds: #status predicted

Query Match 62.5%; Score 192; DB 1; Length 478;
Best Local Similarity 61.8%; Pred. No. 2.5e-16;
Matches 34; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTKPNEETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRINY 55
Db 68 MQRFLGLEMTGKLDNSTLEIVRKPCRGVDSGGFSTFGSPKWRKSHITIRINY 122

RESULT 12

KRTS2

stromelysin 2 (EC 3.4.24.22) precursor - rat
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: B26403; A1775; S26498
R:Breathnach, R.; Matrisian, L.M.; Geanel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A:Reference number: A26403; MUID:87146421; PMID:3547333
A:Accession: B26403
A:Molecule type: mRNA
A:Residues: 1-476 <BRE>
A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57388
A:Note: Intron positions were determined by comparison of the cDNA sequence to genomic s
R:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas
J. Biol. Chem. 267, 1099-1103, 1992
A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ
A:Reference number: A41775; MUID:92112748; PMID:1370458
A:Accession: A41775
A:Molecule type: mRNA
A:Residues: 1-476 <CHA>
A:Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151
A:Note: sequence extracted from NCBI backbone (NCBIP:76184)
R:de Vries, M.W.; Mukherjee, B.B.
Oncogene 7, 109-119, 1992
A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra
A:Reference number: S26498; MUID:92158347; PMID:1741158
A:Accession: S26498
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 31-103, 'L', 241-242, 'QMEEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>
A:Cross-references: EMBL:X64020
C:Genetics:
A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-476/Product: prostromelysin 2 #status predicted <ACT>
F:18-99/Domain: activation peptide #status predicted <ACT>
F:60-264/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-476/Product: stromelysin 2 #status predicted <MAT>
F:283-476/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:120/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 61.9%; Score 190; DB 1; Length 476;
Best Local Similarity 58.2%; Pred. No. 4.5e-16;
Matches 32; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MORFFGLNTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
DB 67 MQKFLGLEMTGLDSDNTVMHMKPRCGVDSGGFSTFGSPKWRKNHISYRINY 121

RESULT 13

A23685

interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)
N:Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
A:Accession: A23685
R:Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge
J. Biol. Chem. 265, 22342-22347, 1990
A:Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormo

A:Reference number: A23685; MUID:91093077; PMID:2176215

A:Accession: A23685
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-466 <QUI>
A:Cross-references: UNIPROT:P23097; GB:M60616; GB:M36452; NID:G203498; PIDN:AAA72124.1; I
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:59-262/Domain: matrix metalloproteinase homology <MMP>
F:273-466/Domain: hemopexin repeat homology <PXN>
F:51,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status I
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F:218/Active site: Glu #status predicted

Query Match 61.6%; Score 189; DB 2; Length 466;

Best Local Similarity 63.6%; Pred. No. 5.8e-16;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MORFFGLNTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
DB 66 MQSFFGLDVTGKLDOPDLDIMRKRPGVDSGGFVYVFPRTLKWSQTNLTIRINY 120

RESULT 14

S29243

interstitial collagenase (EC 3.4.24.7) precursor - mouse
N:Alternate names: matrix metalloproteinase 1 (MMP1)
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S29243
R:Henriet, P.; Rousseau, G.G.; Beckhout, Y.
FEBS Lett. 310, 175-178, 1992
A:Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat c
A:Reference number: S29243; MUID:93011910; PMID:1383028
A:Accession: S29243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <HEN>
A:Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G53604
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:65-268/Domain: matrix metalloproteinase homology <MMP>
F:279-472/Domain: hemopexin repeat homology <PXN>
F:97,223,227,233/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status I
F:223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted
F:224/Active site: Glu #status predicted

Query Match 61.6%; Score 189; DB 2; Length 472;

Best Local Similarity 63.6%; Pred. No. 5.9e-16;
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 MORFFGLNTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
DB 72 MQSFFGLEVTGKLDOPDLDIMRKRPGVDSGGFVYVFPRTLKWSQTNLTIRINY 126

RESULT 15

AS3711

collagenase 3 (EC 3.4.24.-) - human
N:Alternate names: matrix metalloproteinase 13 (MMP13)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: AS3711
R:Preijje, J.M.P.; Diez-Itza, I.; Balbin, M.; Sanchez, L.M.; Blasco, R.; Tollivia, J.; Lopez
J. Biol. Chem. 269, 16766-16773, 1994
A:Title: Molecular cloning and expression of collagenase-3, a novel human matrix metallo
A:Reference number: AS3711; MUID:94266894; PMID:8207000
A:Accession: AS3711
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-471 <PRE>
A:Cross-references: UNIPROT:P45452; GB:X75308; NID:G516385; PIDN:CAA53056.1; PID:G516386
C:Genetics:

A:Gene: GDB:MMP13; CLG3
A:Cross-references: GDB:373966; OMIM:600108
A:Map position: 11q22.2-11q22.3
C:Superfamily: Interstitial collagenase; hemopexin repeat
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:64-267/Domain: matrix metalloproteinase <MMP>
F:278-471/Domain: hemopexin repeat homology <PXN>
F:96,222,236,232/Binding site: zinc, catalytic (Cys, His, His)
F:222,226,232/Binding site: zinc, catalytic (His) (active)
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;
Best Local Similarity 63.6%; Pred. No. 7.9e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy

1 MQRFFGLNVTKPNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTYRINY 55
||| ||| : | : ||| ||| : ||| : ||| |||
D6

71 MOSFGLEVTGKLDDNTLDMMKKPCGVPDGEYVPTTLKWSKMNLTYRINY 125

Search completed: May 27, 2005, 07:13:34
Job time : 20.8013 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 96.25 Seconds
(without alignments)
292.617 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVGKNEETLDM.....LTPGNPKWERTNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 MM08_HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01_RABIT	P13943 oryctolagus
3	231	75.2	469	1 MM01_PIG	P21692 sus scrofa
4	223	72.6	466	1 MM08_RAT	O88766 rattus norv
5	222	72.3	469	1 MM01_HORSE	Q3xs25 equus cabal
6	221	72.0	469	1 MM01_HUMAN	P03956 homo sapien
7	218	71.0	469	1 MM01_BOVIN	P28053 bos taurus
8	201.5	65.6	384	1 MM01_RANCA	Q11133 rana catesb
9	198	64.5	465	2 O8C209	O8C209 mus musculu
10	198	64.5	465	2 O8C230	O8C230 mus musculu
11	198	64.5	478	2 Q6Y405	Q6Y405 canis fami
12	196	63.8	469	1 MM13_XENIA	Q10835 xenopus lae
13	196	63.8	472	2 Q93342	Q93342 gallus gall
14	196	63.8	472	2 Q10833	Q10833 xenopus lae
15	195	63.8	477	1 MM03_HUMAN	P08254 homo sapien
16	195	63.5	476	1 MM10_HUMAN	P09238 homo sapien
17	194	63.2	145	2 Q9N283	Q9N283 bos taurus
18	194	63.2	452	2 Q9TT82	Q9TT82 canis fami
19	193	62.9	476	1 MM10_MOUSE	O55123 mus musculu
20	193	62.9	477	1 MM03_MOUSE	P28862 mus musculu
21	193	62.9	479	2 Q922W6	Q922W6 mus musculu
22	192	62.5	478	1 MM03_RABIT	P28863 oryctolagus
23	190	61.9	465	1 MM08_MOUSE	O70138 mus musculu
24	190	61.9	476	1 MM10_RAT	P07152 rattus norv
25	189	61.6	466	1 MM13_RAT	P23097 rattus norv
26	189	61.6	472	1 MM13_MOUSE	P33435 mus musculu
27	188	61.2	383	2 Q7Z5M0	Q7Z5M0 homo sapien
28	188	61.2	393	2 Q8M1I8	Q8M1I8 felis silve
29	188	61.2	471	1 MM13_HUMAN	P45452 homo sapien
30	188	61.2	471	2 Q6NWN6	Q6NWN6 homo sapien
31	188	61.2	475	1 MM03_RAT	P03957 rattus norv

Q7z5m1 homo sapien
O18927 equus cabal
Q9gm68 sus scrofa
O77656 bos taurus
Q6df35 xenopus tro
O18767 bos taurus
Q98859 cynops pyrr
Q28397 equus cabal
O60882 homo sapien
P79287 sus scrofa
O6dkr9 homo sapien
Q78yxl xenopus lae
O62806 oryctolagus
P57748 mus musculu

ALIGNMENTS

RESULT 1

MM08_HUMAN STANDARD; PRT; 467 AA.
AC P22894;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).
GN Name=MMP8; Synonyms=CLG1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.
RC TISSUE=Neutrophils;
RX MEDLINE=90307647; PubMed=2164002;
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,
RA Spinella D.G., Stevens R.M., Mainardi C.L.;
RT "Human neutrophil collagenase. A distinct gene product with homology
RT to other matrix metalloproteinases";
RL J. Biol. Chem. 265:11421-11424(1990).
RN [2]
RP SEQUENCE OF 21-140.
RC TISSUE=Neutrophils;
RX MEDLINE=90249372; PubMed=2159879;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Characterization and activation of procollagenase from human
RT polymorphonuclear leucocytes. N-terminal sequence determination of the
RT proenzyme and various proteolytically activated forms.";
RL Eur. J. Biochem. 189:295-300(1990).
RN [3]
RP SEQUENCE OF 21-103.
RC TISSUE=Neutrophils;
RX MEDLINE=92111500; PubMed=1662606;
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;
RT "Mercurial activation of human polymorphonuclear leucocyte
RT procollagenase.";
RL Eur. J. Biochem. 202:1223-1230(1991).
RN [4]
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
RC TISSUE=Neutrophils;
RX MEDLINE=91104978; PubMed=2176876;
RA Mallva S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,
RA Birkedal-Hansen H., van Wart H.E.;
RT "Characterization of 58-kilodalton human neutrophil collagenase:
RT comparison with human fibroblast collagenase.";
RL Biochemistry 29:10628-10634(1990).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=90380298; PubMed=2169256;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";

RL Biol. Chem. Hoppe-Seyler 371:295-304 (1990).
 RN [6]
 RP MEDLINE=91000455; PubMed=2169766;
 RX Kraeuper V., Kraeuper S., Reinke H., Tschesche H.;
 RA Biol. Chem. Hoppe-Seyler 371:733-733 (1990).
 RN [7]
 RP Cysteine-Switch Mechanism.
 RC TISSUE=Neutrophils;
 RX Blaesser J., Triebel S., Reinke H., Tschesche H.;
 RA "Formation of a covalent Hg-Cys-bond during mercurial activation of
 RT PNL procollagenase gives evidence of a cysteine-switch mechanism.";
 RL FEBS Lett. 313:59-61 (1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
 RX MEDLINE=94185631; PubMed=8137810;
 RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
 RT "The X-ray crystal structure of the catalytic domain of human
 RT neutrophil collagenase inhibited by a substrate analogue reveals the
 RT essentials for catalysis and specificity.";
 RL EMBO J. 13:1263-1269 (1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
 RX MEDLINE=94139930; PubMed=8307185; DOI=10.1016/0014-5793(94)80370-6;
 RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
 RA Tschesche H., Bode W.;
 RT "Structural implications for the role of the N terminus in the
 RT 'superactivation' of collagenases. A crystallographic study.";
 RL PDBS Lett. 338:227-233 (1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
 RX MEDLINE=95384762; PubMed=7656015;
 RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
 RA Oorofleh M.W., Banks T.M., Rubin B.;
 RT "Structure of human neutrophil collagenase reveals large S1'
 RT specificity pocket.";
 RL Nat. Struct. Biol. 1:119-123 (1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
 RX MEDLINE=97390108; PubMed=9249047;
 RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
 RA Bode W., Gomis-Rueth F.-X.;
 RT "1.8-A crystal structure of the catalytic domain of human neutrophil
 RT collagenase (matrix metalloproteinase-8) complexed with a
 RT peptidomimetic hydroxamate primed-side inhibitor with a distinct
 RT selectivity profile.";
 RL Eur. J. Biochem. 247:356-363 (1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
 RX MEDLINE=98318039; PubMed=9655333;
 RA Brandstetter H., Engl R.A., von Roeder E.G., Moroder L., Huber R.,
 RA Bode W., Grams F.;
 RT "Structure of malonic acid-based inhibitors bound to human neutrophil
 RT collagenase. A new binding mode explains apparently anomalous data.";
 RL Protein Sci. 7:1303-1309 (1998).
 CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
 CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
 CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
 CC type III collagen more slowly than type I.
 CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
 CC -!- ENZYME REGULATION: Cannot be activated without removal of the
 CC activation peptide.
 CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
 CC -!- TISSUE SPECIFICITY: Neutrophils.
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 1 hemoexin-like domain.
 CC -----
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 CC -----
 CC EMBL: J05556; AAA88021.1; -
 CC PIR: A37073; KCHUN.
 DR PDB: 1A85; X-ray; A=105-262.
 DR PDB: 1A86; X-ray; A=105-262.
 DR PDB: 1B2S; X-ray; A=99-263.
 DR PDB: 1I73; X-ray; A=100-262.
 DR PDB: 1I76; X-ray; A=100-262.
 DR PDB: 1JAN; X-ray; A=99-262.
 DR PDB: 1JAO; X-ray; A=100-262.
 DR PDB: 1JAP; X-ray; A=100-262.
 DR PDB: 1JQA; X-ray; A=100-262.
 DR PDB: 1JH1; X-ray; A=105-262.
 DR PDB: 1JH9; X-ray; A=100-262.
 DR PDB: 1KBC; X-ray; A/B=99-262.
 DR PDB: 1MWB; X-ray; @=100-262.
 DR PDB: 1MNC; X-ray; @=101-263.
 DR MEROPS; M10.002; -
 DR Genew; HGNC:7175; MMP8.
 DR MIM; 120355; -
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008130; F:neutrophil collagenase activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding; TAS.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR000585; Hemoexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGSD-like.
 DR Pfam; PF00045; Hemoexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PRO0138; MATRXIN.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 DR 3D-structure; Calcium-Binding; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-Binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 20
 FT PROPEP 21 100 Activation peptide.
 FT CHAIN 101 467 Neutrophil collagenase.
 FT DOMAIN 276 467 Hemoexin-like.
 FT SITE 91 91 Cysteine switch.
 FT METAL 157 157 Calcium 1.
 FT METAL 167 167 Zinc 1.
 FT METAL 169 169 Zinc 1.
 FT METAL 174 174 Calcium 2.
 FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
 FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
 FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
 FT METAL 182 182 Zinc 1.
 FT METAL 189 189 Calcium 1 (via carbonyl oxygen).
 FT METAL 191 191 Calcium 1 (via carbonyl oxygen).
 FT METAL 193 193 Calcium 1.
 FT METAL 195 195 Zinc 1.
 FT METAL 197 197 Calcium 2.
 FT METAL 200 200 Calcium 2.
 FT METAL 217 217 Zinc 2 (catalytic).
 FT ACT SITE 218 218 Zinc 2 (catalytic).
 FT METAL 221 221 Zinc 2 (catalytic).
 FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 286 similarity).
 FT METAL 378 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 425 similarity).
 FT METAL 54 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 73 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 112 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 204 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
 FT DISULFID 279 464 Probable.

Query Match 100.0%; Score 307; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-29; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPRCGVPSGGFMTFGNPKWERTNLTIRYNY 55
 |||||
 Db 66 MORFFGLNVTGKNEETLDMKKPRCGVPSGGFMTFGNPKWERTNLTIRYNY 120
 |||||

RESULT 2

MM01_RABIT STANDARD; PRT; 468 AA.

AC PI3943;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 DE metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=88077876; PubMed=2825772;
 RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
 RT "A gene for rabbit synovial cell collagenase: member of a family of
 RT metalloproteinases that degrade the connective tissue matrix.";
 RL Biochemistry 26:6156-6165(1987).
 RN [2]
 RP SEQUENCE OF 449-468 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=87029174; PubMed=3021384;
 RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
 RA Brinckerhoff C.E.;
 RT "Homology between exon-containing portions of rabbit genomic clones
 RT for synovial cell collagenase and human foreskin and synovial cell
 RT mRNAs.";
 RL Coll. Relat. Res. 6:239-248(1986).
 CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where p1' is a
 CC hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC similarity).
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.

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 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC ENBL; M17823; AAB88016.1; -.
 CC ENBL; M17820; AAB88016.1; JOINED.
 CC ENBL; M17821; AAB88016.1; JOINED.
 CC ENBL; M17822; AAB88016.1; JOINED.
 CC ENBL; M19240; AAB88016.1; JOINED.
 CC ENBL; M25663; AAA31203.1; -.

DR PIR; A27500; KCRBI.
 DR HSSP; P03956; 1CGL.
 DR MEROPS; M10.001; -.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR009070; PGBD like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.

FT SIGNAL	1	18	Activation peptide.
FT PROPEP	19	98	Interstitial collagenase.
FT CHAIN	99	468	Hemopexin-like.
FT DOMAIN	274	468	Cysteine switch (Potential).
FT SITE	91	91	Calcium 1 (By similarity).
FT METAL	123	123	Calcium 2 (By similarity).
FT METAL	157	157	Zinc 1 (By similarity).
FT METAL	167	167	Zinc 1 (By similarity).
FT METAL	169	169	Calcium 3 (By similarity).
FT METAL	174	174	Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL	175	175	Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL	177	177	Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL	179	179	Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL	182	182	Zinc 1 (By similarity).
FT METAL	189	189	Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL	191	191	Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL	193	193	Calcium 2 (By similarity).
FT METAL	195	195	Zinc 1 (By similarity).
FT METAL	197	197	Calcium 3 (By similarity).
FT METAL	198	198	Calcium 1 (By similarity).
FT METAL	200	200	Calcium 3 (By similarity).
FT METAL	217	217	Zinc 2 (catalytic) (By similarity).
FT ACT_SITE	218	218	By similarity.
FT METAL	221	221	Zinc 2 (catalytic) (By similarity).
FT METAL	227	227	Zinc 2 (catalytic) (By similarity).
FT METAL	284	284	Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL	328	328	Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL	377	377	Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL	426	426	Calcium 4 (via carbonyl oxygen) (By similarity).
FT CARBOHYD	119	119	N-linked (GlcNAc...) (Probable).
FT DISULFID	277	465	By similarity.
SQ SEQUENCE	468 AA;	53739 MW;	DA9053891995288C CRC64;

Query Match 75.9%; Score 233; DB 1; Length 468;
 Best Local Similarity 74.5%; Pred. No. 3.7e-20;
 Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPRCGVPSGGFMTFGNPKWERTNLTIRYNY 55
 |||||
 Db 66 MORFFGLNVTGKNEETLDMKKPRCGVPSGGFMTFGNPKWERTNLTIRYNY 120
 |||||

RESULT 3
 MM01_PIG

ID AC MM01_PIG STANDARD; PRT; 469 AA.
 DT P21632;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 DE metalloproteinase-1) (MMP-1).
 GN Name:MMP1;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91333421; PubMed=1651440;
 RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
 RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
 RT modulation of expression of RNA in vitro by various cytokines.";
 RL Matrix 11:161-167(1991).
 RN [2]
 RP SEQUENCE OF 25-469 FROM N.A.
 RX TISSUE=Synovial cell;
 RC MEDLINE=91067477; PubMed=2174547;
 RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
 RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
 RT obtained by PCR.";
 RL Nucleic Acids Res. 18:6703-6703(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
 RX MEDLINE=96173003; PubMed=8590015; DOI=10.1016/S0969-2126(01)00186-5;
 RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
 RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
 RT "Structure of full-length porcine synovial collagenase reveals a C-
 RT terminal domain containing a calcium-linked, four-bladed beta-
 RT propeller.";
 RL Structure 3:541-549(1995).
 RN [4]
 RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
 RX MEDLINE=95142635; PubMed=7840605; DOI=10.1006/abbi.1995.1018;
 RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
 RA O'Hare M.C.;
 RT "Recombinant porcine collagenase: purification and autolysis.";
 RL Arch. Biochem. Biophys. 316:123-127(1995).
 CC -I- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -I- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where P1' is a
 CC hydrophobic residue.
 CC -I- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
 CC -I- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -I- PTM: Undergoes autocatalytic cleavage to produce a N-terminal fragment
 CC having reduced collagenolytic activity.
 CC -I- SIMILARITY: Belongs to the peptidase M10A family.
 CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 DR EMBL; X54724; CAA38526.1; -;
 DR PIR; S15986; KCPGI.
 DR PDB; 1FBL; X-ray; @=100-469.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.

DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR005070; PGSD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZNMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
 KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19 Activation peptide.
 FT PROPEP 20 99 Interstitial collagenase.
 FT CHAIN 100 469 18 kDa interstitial collagenase.
 FT CHAIN 100 258 Hemopexin-like.
 FT DOMAIN 275 469 Cysteine switch (Potential).
 FT SITE 92 92 Cleavage (autolytic).
 FT SITE 258 259 Calcium 1.
 FT METAL 124 124 Calcium 2.
 FT METAL 158 158 Calcium 1.
 FT METAL 168 168 Zinc 1.
 FT METAL 170 170 Zinc 1.
 FT METAL 175 175 Calcium 3.
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
 FT METAL 183 183 Zinc 1.
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
 FT METAL 194 194 Calcium 2.
 FT METAL 196 196 Zinc 1.
 FT METAL 198 198 Calcium 3.
 FT METAL 199 199 Calcium 1.
 FT METAL 201 201 Calcium 3.
 FT METAL 218 218 Zinc 2 (catalytic).
 FT ACT_SITE 219 219 Zinc 2 (catalytic).
 FT METAL 222 222 Zinc 2 (catalytic).
 FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
 FT DISULFID 278 466 N-linked (GlcNAc..)(Potential).
 FT CARBOHYD 120 120
 FT STRAND 101 102
 FT TURN 104 105
 FT STRAND 113 118
 FT TURN 123 124
 FT TURN 127 142
 FT HELIX 127 142
 FT TURN 143 144
 FT STRAND 148 152
 FT STRAND 159 164
 FT STRAND 182 184
 FT TURN 193 193
 FT STRAND 195 198
 FT TURN 199 200
 FT STRAND 204 204
 FT STRAND 211 211
 FT HELIX 212 223
 FT TURN 224 225
 FT STRAND 226 227
 FT TURN 232 233
 FT TURN 235 236
 FT HELIX 250 260
 FT TURN 277 278
 FT TURN 280 281
 FT TURN 286 290
 FT TURN 291 292


```
Matches 39; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 1 MORFFGLVNTGKPNETLDMKKPCGVPDGGFMLTGPCNPKWERTNLTIRNY 55
    ||||| ||| : : : : ||||| : : : : ||||| : : : : ||||| :
Db 67 MORFFGLPTGKPDAAITIMEKPCGVPDGGDFLLTTPGSPKWTHTNLTIRINH 121
    ||||| ||| : : : : ||||| : : : : ||||| : : : : ||||| :

RESULT 5
MM01_HUMAN
ID MM01_HUMAN STANDARD; PRT; 469 AA.
AC Q9XSZ5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]_
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT "Cloning and expression of equine matrix metalloproteinase 1
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagenous types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where p1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC -----
CC EMBL; AF148882; AAD38030.1; -.
CC HSP; P03956; 1AYK.
CC MEROPS; M10_001; -.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept M_2n BS.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR009070; PGD like.
CC Pfam; PF00045; Hemopexin; 4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00138; MATRILIX.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Extracellular matrix;
CC Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
CC Zymogen.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
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FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 Cysteine switch (Potential).
FT METAL 124 Calcium 1 (By similarity).
FT METAL 158 Calcium 2 (By similarity).
FT METAL 168 Zinc 1 (By similarity).
FT METAL 170 Zinc 1 (By similarity).
FT METAL 176 Calcium 3 (By similarity).
FT METAL 176 Calcium 3 (via carbonyl oxygen) (By
FT METAL 178 similarity).
FT METAL 178 Calcium 3 (via carbonyl oxygen) (By
FT METAL 180 similarity).
FT METAL 180 Calcium 3 (via carbonyl oxygen) (By
FT METAL 183 similarity).
FT METAL 190 Zinc 1 (By similarity).
FT METAL 192 Calcium 2 (via carbonyl oxygen) (By
FT METAL 192 similarity).
FT METAL 194 Calcium 2 (By similarity).
FT METAL 196 Zinc 1 (By similarity).
FT METAL 198 Calcium 3 (By similarity).
FT METAL 199 Calcium 1 (By similarity).
FT METAL 201 Calcium 3 (By similarity).
FT METAL 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 By similarity.
FT METAL 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 Zinc 2 (catalytic) (By similarity).
FT METAL 285 Calcium 4 (via carbonyl oxygen) (By
FT METAL 329 similarity).
FT METAL 329 Calcium 4 (via carbonyl oxygen) (By
FT METAL 378 similarity).
FT METAL 427 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 278 By similarity.
SQ SEQUENCE 469 AA; 54001 MW; AE86760AB2C529CA CRC64;

Query Match 72.3%; Score 222; DB 1; Length 469;
Best Local Similarity 70.9%; Pred. No. 8.4e-19;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MORFFGLVNTGKPNETLDMKKPCGVPDGGFMLTGPCNPKWERTNLTIRNY 55
Db 67 MORFFGLKVTGKPDAAITLNMVKQPCGVPDVAEFTVTEGNPRWHTLTIRIENY 121

RESULT 6
MM01_HUMAN
ID MM01_HUMAN STANDARD; PRT; 469 AA.
AC P03956; P08156;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90352587; PubMed=2167156;
RA Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,
RA Stetler-Stevenson W.G.;
RT "Cloning and characterization of human tumor cell interstitial
RT collagenase.";
RL Cancer Res. 50:5431-5437(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
```

RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
sequence analysis";
RL Biochem. J. 240:913-916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196089; PubMed=3009463;
RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,
RT Eisen A.Z.;
RA "Human fibroblast collagenase. Complete primary structure and homology
to an oncogene transformation-induced rat protein.";
RL J. Biol. Chem. 261:6600-6605(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Pederspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdil O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.W., Green E.D., Dickson M.C.,
RA Blakeley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Dellus H., Rahmsdorf H.J.,
RA Herrlich P.;
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
collagenase gene is mediated by an inducible enhancer element located
in the 5'-flanking region";
RL Mol. Cell. Biol. 7:2256-2266(1987).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RX TISSUE=Synovial cell;
RA MEDLINE=87109799; PubMed=3027129;
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
RT "Molecular cloning of human synovial cell collagenase and selection of
a single gene from genomic DNA";
RL J. Clin. Invest. 79:542-546(1987).
RN [8]
RP SEQUENCE OF 100-112 AND 270-287.
RX TISSUE=Fibroblast;
RA MEDLINE=90104231; PubMed=2557822;
RA Clark I.M., Cawston T.E.;
RT "Fragments of human fibroblast collagenase. Purification and
characterization";
RL Biochem. J. 263:201-206(1989).
RN [9]
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrrow J.H.;
RT "Human fibroblast collagenase contains an amino acid sequence
homologous to the zinc-binding site of Serratia protease.";
RL J. Biol. Chem. 262:5943-5943(1987).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.;
RT "Structure of the catalytic domain of human fibroblast collagenase
complexed with an inhibitor";
RL Nat. Struct. Biol. 1:106-110(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
complexed to itself";
RL Biochemistry 33:8207-8217(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.;
RT "Structure of the catalytic domain of fibroblast collagenase complexed
with an inhibitor";
RL Science 263:375-377(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
RT "1.56-A structure of mature truncated human fibroblast collagenase";
RN Proteins 19:98-109(1994).
RL [14]
RP STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219; DOI=10.1021/bi972181w;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.;
RT "High-resolution solution structure of the inhibitor-free catalytic
fragment of human fibroblast collagenase determined by
multidimensional NMR";
RL Biochemistry 37:1495-1504(1998).
RN [15]
RP FUNCTION: Cleaves collagens of types I, II, and III at one site in
the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
collagen. Cleavage of the triple helix of collagen at about three-
quarters of the length of the molecule from the N-terminus, at
775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
substrates and alpha-macroglobulins at bonds where P1' is a
hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -1- ENZYME REGULATION: Can be activated without removal of the
activation peptide.
CC -1- DOMAIN: There are two distinct domains in this protein; the
catalytic N-terminal, and the C-terminal which is involved in
substrate specificity and in binding TIMP (tissue inhibitor of
metalloproteinases).
CC -1- PTM: Undergoes autocatalytic cleavage to two major forms (22 kDa and
27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
kDa form. The 27 kDa form has no activity while the 22/25 kDa form
can act as activator for collagenase.
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05231; CAA28858.1; -.


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FT METAL 329 329 similarity).
FT Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT DISULFID 278 466 By similarity.
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CONFLICT 22 23 AT -> FP (in Ref. 2).
FT CONFLICT 30 30 D -> L (in Ref. 2).
FT CONFLICT 35 36 KK -> LL (in Ref. 2).
FT CONFLICT 85 85 N -> F (in Ref. 2).
FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
FT CONFLICT 113 113 N -> D (in Ref. 2).
SQ SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;

Query Match 71.08; Score 218; DB 1; Length 469;
Best Local Similarity 70.94; Pred. No. 2.6e-18;
Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTYRIY 55
DB 67 MQRFFGLVNTGKPDATLNVKQPRCGVDPVAPVLPFGKSWCNTLTYRIY 121

RESULT 8
MM01_RANCA STANDARD; PRT; 384 AA.
ID MM01_RANCA
AC Q1133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (TCL).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8400;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=95071832; PubMed=7981043;
RA Oofusa K., Yomori S., Yoshizato K.;
RT "Regionally and hormonally regulated expression of genes of collagen
RT and collagenase in the anuran larval skin.";
RL Int. J. Dev. Biol. 38:345-350(1994).
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; S75623; AAB32661.1; --
DR PSR; I51267; I51267.
DR HSSP; P21692; 1FBL.

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DR MEROPS; M10.001; --
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGHD_like.
DR Pfam; PF00413; Hemopexin; 2.
DR Pfam; PF03933; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE NEG.
DR PROSITE; PS00024; HEMOPEXIN; FALSE NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 25 Potential.
FT PROPEP 26 88 Activation peptide (Potential).
FT CHAIN 89 384 Interstitial collagenase.
FT DOMAIN 239 384 Hemopexin-like.
FT SITE 81 81 Cysteine switch (Potential).
FT METAL 113 113 Calcium 1 (By similarity).
FT METAL 129 129 Calcium 2 (By similarity).
FT METAL 139 139 Zinc 1 (By similarity).
FT METAL 141 141 Zinc 1 (By similarity).
FT METAL 146 146 Calcium 3 (By similarity).
FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Calcium 3 (By similarity).
FT METAL 170 170 Calcium 1 (By similarity).
FT METAL 172 172 Calcium 3 (By similarity).
FT METAL 189 189 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 190 190 By similarity.
FT METAL 193 193 Zinc 2 (catalytic) (By similarity).
FT METAL 199 199 Zinc 2 (catalytic) (By similarity).
FT METAL 249 249 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 277 277 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 347 347 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT DISULFID 242 381 By similarity.
SQ SEQUENCE 384 AA; 43582 MW; ASB5E2FB32239DF CRC64;

Query Match 65.6%; Score 201.5; DB 1; Length 384;
Best Local Similarity 65.5%; Pred. No. 2.3e-16;
Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MQRFFGLVNTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTYRIY 55
DB 57 LKQFFGLVNTGKPDATLNVKQSTCGVDPVGYLTPGNPRWENTHLYRIY 110

RESULT 9
Q8C209 PRELIMINARY; PRT; 465 AA.
AC Q8C209;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-

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RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muranatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089381; BAC40862.1; -.
DR HSSP; P22894; IJAP.
DR MGD; MGI:1202395; Mmp8.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 465 AA; 53114 MW; F80522831AACB4B2 CRC64;

Query Match 64.5%; Score 198; DB 2; Length 465;
Best Local Similarity 65.5%; Pred. No. 7; 7e-16;
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTYYRNY 55
Db 66 MQRFFSLAETGKLDATMGIMEMPRCGVPSGGFLLTPGSPKWTHTNLTYYRIINH 120

RESULT 11
Q6Y4Q5 Q6Y4Q5 PRELIMINARY; PRT; 478 AA.
AC Q6Y4Q5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Name=MMP3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY183143; AA063580.1; -.
DR HSSP; P08254; I83D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

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DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;

Query Match 64.5%; Score 198; DB 2; Length 478;
Best Local Similarity 63.6%; Pred. No. 8e-16;
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTYYRNY 55
Db 67 MQRFLGLEVTGKVDSDTLAMRRPRCGVPSGGFLLTPGSPKWTHTNLTYYRIMY 121

RESULT 12
M13_XENLA STANDARD; PRT; 469 AA.
AC Q10835;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Collagenase 3 precursor (EC 3.4.24.-) (Matrix metalloproteinase-13)
DE (MMP-13) (Fragment).
GN Name=MMP13;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tail;
RA Fini M.E., Scott S., Wang Z., Brown D.D.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Degrades collagen type I.
CC -!- COFACTOR: Binds 2 zinc ions and 5 calcium ions per subunit (By
CC similarity).
CC -!- DEVELOPMENTAL STAGE: Up-regulated by thyroid hormone in tadpoles
CC during tail resorption.
CC -!- MISCELLANEOUS: The Xenopus genome contains two genes coding for
CC very similar enzymes: MMP-13 and MMP-13A.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; L49412; AAA83996.1; -.
DR HSSP; P33435; ICKV.
DR MEROPS; M10.013; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.

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DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
DR Calcium-binding; Collagen degradation;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT METAL 1 1
FT NON TER <1 17
FT SIGNAL 18 100
FT PROPEP 18 100
FT CHAIN 101 469
FT DOMAIN 279 469
FT SITE 94 94
FT METAL 160 160
FT METAL 170 170
FT METAL 172 172
FT METAL 177 177
FT METAL 178 178
FT METAL 185 185
FT METAL 192 192
FT METAL 194 194
FT METAL 196 196
FT METAL 198 198
FT METAL 203 203
FT METAL 220 220
FT ACT SITE 221 221
FT METAL 224 224
FT METAL 230 230
FT METAL 289 289
FT METAL 291 291
FT METAL 333 333
FT METAL 335 335
FT METAL 381 381
FT METAL 383 383
FT METAL 430 430
FT METAL 432 432
FT DISULFID 282 469
FT CARBOHYD 115 115
FT CARBOHYD 150 150
SQ SEQUENCE 469 AA; EF02BF4BEC429D77 CRC64;

Query Match 63.8%; Score 196; DB 1; Length 469;
Best Local Similarity 67.3%; Pred. No. 1.4e-15;
Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 69 MQSFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 123

RESULT 13
O93342 PRELIMINARY; PRT; 472 AA.
ID AC O93342
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Matrix metalloproteinase.
OS Gallus gallus (Chicken).

Query Match 63.8%; Score 196; DB 1; Length 469;
Best Local Similarity 67.3%; Pred. No. 1.4e-15;
Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 69 MQSFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 123

RESULT 13
O93342 PRELIMINARY; PRT; 472 AA.
ID AC O93342
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Matrix metalloproteinase.
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang M., Kurkinen M.;
RT "Cloning of a novel matrix metalloproteinase (MMP) from chicken
RT embryo fibroblasts.";
RL J. Biol. Chem. 0:0-0(1998).
DR EMBL; AF062392; AAC33733.1; -.
DR HSSP; P45452; 830C.
DR MEROPS; M10.027; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR PRINTS; PR03933; Peptidase M10_N; 1.
DR SMART; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 472 AA; 53254 MW; AAL35CB3F67C868 CRC64;

Query Match 63.8%; Score 196; DB 2; Length 472;
Best Local Similarity 69.1%; Pred. No. 1.4e-15;
Matches 38; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 MQRFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 72 MQRFFGLVNTGKNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 124

RESULT 14
Q10833 PRELIMINARY; PRT; 472 AA.
ID Q10833
AC Q10833
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-3.
GN Name=Gene A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312514; PubMed=8700860; DOI=10.1073/pnas.93.5.1924;
RA Brown D.D., Wang Z., Furrow J.D., Kanamori A., Schwartzman R.A.,
RA Remo B.F., Pinder A.;
RT "The thyroid hormone-induced tail resorption program during Xenopus
RT laevis metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
DR EMBL; U01824; AAC59870.1; -.
DR HSSP; P33435; 1CXV.
DR MEROPS; M10.013; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.

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RA Trepod C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A.,
RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.;
RT "Structural characterizations of nonpeptidic thiadiazole inhibitors of
RT matrix metalloproteinases reveal the basis for stromelysin
RT selectivity.";
RL Protein Sci. 7:2118-2126(1998).
RN [14]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.
RP MEDLINE=20013067; PubMed=10543949; DOI=10.1006/jmbi.1999.3147;
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RA Barnet B.L.;
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A
RT resolution: inhibitor-induced conformational changes.";
RL J. Mol. Biol. 293:545-557(1999).
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RP MEDLINE=99349695; PubMed=10422833;
RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwine D.F.,
RA Purchase C.F. II, White A.D., Dhanaraj V., Roth B.D., Johnson L.L.,
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RT nonpeptide inhibitors: implications for inhibitor selectivity.";
RL Protein Sci. 8:1455-1462(1999).
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RX STRUCTURE BY NMR OF 100-272.
RP MEDLINE=98434377; PubMed=9760240; DOI=10.1021/bi981328w;
RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.;
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RT complexed to a potent, nonpeptidic inhibitor.";
RL Biochemistry 37:14048-14056(1998).
CC !- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
CC proteoglycans. Activates procollagenase.
CC !- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3',
CC are hydrophobic residues.
CC !- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC !- SIMILARITY: Belongs to the peptidase M10A family.
CC !- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; X05232; CAA28859.1; -;
DR EMBL; J03209; AAA36321.1; -;
DR EMBL; U78045; AAB36942.1; -;
DR EMBL; AF405705; AAK95247.1; -;
DR PIR; A28156; KCHUS1.
DR PDB; 1B3D; X-ray; A/B=100-272.
DR PDB; 1B8Y; X-ray; A=100-266.
DR PDB; 1B1W; X-ray; A/B=100-272.
DR PDB; 1BM6; NMR; @=100-272.
DR PDB; 1BQO; X-ray; A/B=100-272.
DR PDB; 1C3I; X-ray; A/B=100-272.
DR PDB; 1C8T; X-ray; A/B=103-269.
DR PDB; 1CAQ; X-ray; A=100-267.
DR PDB; 1C1Z; X-ray; A=100-267.
DR PDB; 1CQR; X-ray; A/B=100-272.
DR PDB; 1DSJ; X-ray; A/B=100-272.
DR PDB; 1D7X; X-ray; A/B=100-272.
DR PDB; 1D8F; X-ray; A/B=100-272.
DR PDB; 1D8M; X-ray; A/B=100-272.
DR PDB; 1G05; X-ray; A/B=100-272.
DR PDB; 1G49; X-ray; A/B=100-272.
DR PDB; 1G4K; X-ray; A/B/C=100-267.
DR PDB; 1HFS; X-ray; @=105-264.
DR PDB; 1HY7; X-ray; A/B=100-272.
DR PDB; 1MLW; Model; A=100-268.
DR PDB; 1OO9; NMR; A=100-267.

DR PDB; 1QIA; X-ray; A/B/C/D=106-267.
DR PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR PDB; 1SLM; X-ray; @=18-272.

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Best Local Similarity 63.6%; Pred. No. 1.4e-15;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
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Db 67 MQRFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKWKTHLTIRVNY 121

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